

00431PHRM293.ST25  
SEQUENCE LISTING

<110> Vogeli, Gabriel  
Huff, Rita  
Sejlitz, Torsten  
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Slightom, Jerry  
Schellin, Kathleen  
Bannigan, Chris  
Ruff, Valerie  
Kaytes, Paul  
Wood, Linda  
Parodi, Luis  
Hiebsch, Ronald

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&lt;170&gt; PatentIn version 3.0

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Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala  
 35 40 45

Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp  
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Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu  
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Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val  
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Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg  
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Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly  
 115 120 125

Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro  
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Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro  
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Ala Met Leu Leu Phe Val Phe Tyr Cys Asp Met Leu Lys Ile Ala  
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Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met  
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Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu  
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Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro  
 225 230 235 240

Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu  
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Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser  
 260 265 270

Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu

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Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe  
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Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu  
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Ala Tyr Ser Ala Glu Leu Arg Thr Arg Ala Ser Gly Val Leu Leu Val  
 35 40 45

Asn Leu Ser Leu Gly His Leu Leu Leu Ala Ala Leu Asp Met Pro Phe  
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Thr Leu Leu Gly Val Met Arg Gly Arg Thr Pro Ser Ala Pro Gly Ala  
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Cys Gln Val Ile Gly Phe Leu Asp Thr Phe Leu Ala Ser Asn Ala Ala  
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Leu Ser Val Ala Ala Leu Ser Ala Asp Gln Trp Leu Ala Val Gly Phe  
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Pro Leu Arg Tyr Ala Gly Arg Leu Arg Pro Arg Tyr Ala Gly Leu Leu  
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Leu Gly Cys Ala Trp Gly Gln Ser Leu Ala Phe Ser Gly Ala Ala Leu  
130 135 140

Gly Cys Ser Trp Leu Gly Tyr Ser Ser Ala Phe Ala Ser Cys Ser Leu  
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Arg Leu Pro Pro Glu Pro Glu Arg Pro Arg Phe Ala Ala Phe Thr Ala  
165 170 175

Thr Leu His Ala Val Gly Phe Val Leu Pro Leu Ala Val Leu Cys Leu  
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Asp Thr Val Thr Met Lys Ala Leu Ala  
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Tyr Leu Leu Cys Thr Ala Ser Val Tyr Asn Ile Val Leu Ile Ser Tyr

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45

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Leu Phe Ser Leu Trp Val Leu Cys Arg Arg Met Gly Pro Arg Ser Pro  
 35 40 45

Ser Val Ile Phe Met Ile Asn Leu Ser Val Thr Asp Leu Met Leu Ala  
 50 55 60

Ser Val Leu Pro Phe Gln Ile Tyr Tyr His Cys Asn Arg His His Trp  
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Val Phe Gly Val Leu Cys Asn Leu Val Val Thr Val Ala Phe Tyr Ala  
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Asn Met Tyr Ser Ser Ile Leu Thr Met Thr Cys Ile Ser Val Glu Arg

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Phe Leu Gly Ile Leu Tyr Pro Leu Ser Ser Lys Arg Trp Arg Arg Arg  
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Arg Tyr Ala Val Ala Ala Cys Ala Gly Thr Trp Leu Leu Leu Leu Thr  
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gcacgggagg gaggcgtctt cgtggcactc actgcgtccg tgctgagcct octggcattc 180  
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Lys Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu Gly Gly Val Phe Val  
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Ala Leu Thr Ala Ser Val Leu Ser Leu Leu Gly Ile Ala Leu Glu Arg  
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Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Met Ile Cys Leu  
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Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His Trp Ala Phe Gly  
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Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala Met Asn Arg Ala  
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Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp Arg Tyr Phe Lys  
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Val Val His Pro His His Ala Val Asn Thr Ile Ser Thr Arg Val Ala  
 100 105 110

Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile Leu Gly Thr Val  
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Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu Thr Ala Val Ser  
 130 135 140

Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp His Asp Ile Met  
 145 150 155 160

Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile Leu Phe Cys Ser  
 165 170 175

Phe Lys Ile Val Trp Ser Leu Arg Arg Gln Gln Leu Ala Arg Gln  
 180 185 190

Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val Val Ala Ile Val  
 195 200 205

Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg Leu Tyr Phe Leu  
 210 215 220

Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val His Gly Ala Leu  
 225 230 235 240

His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met Leu Asp Pro Leu  
 245 250 255

Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe Tyr Asn Lys Leu  
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Arg Trp Pro Phe Gly Glu Leu Leu Cys Lys Leu Val His Phe Leu Phe  
35 40 45

Tyr Ile Asn Leu Tyr Gly Ser Ile Leu Leu Leu Thr Cys Ile Ser Val  
50 55 60

His Gln Phe Leu Gly Val Cys His Pro Leu Cys Ser Leu Pro Tyr Arg  
65 70 75 80

Thr Arg Arg His Ala Trp Leu Gly Thr Ser Thr Thr Trp Ala Leu Val  
85 90 95

Val Leu Gln Leu Leu Pro Thr Leu Ala Phe Ser His Thr Asp Tyr Ile  
100 105 110

Asn Gly Gln Met Ile Trp Tyr Asp Met Thr Ser Gln Glu Asn Phe Asp  
115 120 125

Arg Leu Phe Ala Tyr Gly Ile Val Leu Thr Leu Ser Gly Phe Leu Ser  
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Leu Leu Gly His Phe Gly Val Leu Phe Thr Asp Gly Gln Glu Pro Asp  
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Xaa	Xaa	Xaa	Lys	Arg	Arg	Lys	Met	Asp	Phe	Leu	Leu	Val	Gln	Leu	Ala
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Leu Val Val Leu Ile Ala Leu Glu Arg Arg Arg Ala Val Arg Leu Pro  
 100 105 110

His Gly Arg Pro Leu Pro Ala Arg Ala Leu Ala Ala Leu Gly Trp Leu  
 115 120 125

Leu Ala Leu Leu Leu Ala Arg Gly Ser Gly Phe Val Val Arg Tyr Xaa  
 130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser Leu Gln Pro Gly  
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 165 170 175

Ile Phe Ala Leu Leu Gln Arg Trp His Val Gln Val Tyr Ala Phe Tyr  
 180 185 190

Glu Ala Val Ala Gly Phe Val Ala Pro Val Lys Ile Met Gly Val Ala  
 195 200 205

Cys Gly His Leu Leu Ser Val Trp Trp Arg His Arg Leu Lys Ala Pro  
 210 215 220

Ala Gly Ala Ala Ala Trp Ser Ala Ser Pro Gly Gly Ala Arg Ala Pro  
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Ser Ala Met Pro Arg Ala Lys Val Gln Ser Leu Lys Met Ser Gln Leu  
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Leu Gly Leu Leu Phe Val Gly Cys Glu Leu Pro Phe Ala Asp Arg Leu  
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<210> 18  
 <211> 249  
 <212> PRT  
 <213> H.Sapiens

<400> 18

Ser	Gly	Met	Glu	Lys	Leu	Gln	Asn	Ala	Ser	Trp	Ile	Tyr	Gln	Gln	Lys
1					5				10				15		
Leu	Glu	Asp	Pro	Phe	Gln	Lys	His	Leu	Asn	Ser	Thr	Glu	Glu	Tyr	Leu
				20				25				30			
Ala	Phe	Leu	Cys	Gly	Pro	Arg	Arg	Ser	His	Phe	Phe	Leu	Pro	Val	Ser
					35			40				45			
Val	Val	Tyr	Val	Pro	Ile	Phe	Val	Val	Gly	Val	Ile	Gly	Asn	Val	Leu
					50			55			60				
Val	Cys	Leu	Val	Ile	Leu	Gln	His	Gln	Ala	Met	Lys	Thr	Pro	Asn	Thr
					65			70			75			80	
Tyr	Tyr	Leu	Phe	Ser	Leu	Ala	Val	Ser	Asp	Leu	Leu	Val	Leu	Leu	
					85			90				95			
Gly	Met	Pro	Leu	Glu	Val	Tyr	Glu	Met	Trp	Arg	Asn	Tyr	Pro	Phe	Leu
					100			105				110			
Phe	Gly	Pro	Val	Gly	Cys	Tyr	Phe	Lys	Thr	Ala	Leu	Phe	Glu	Thr	Val
					115			120			125				
Cys	Phe	Ala	Ser	Ile	Leu	Ser	Ile	Thr	Thr	Val	Ser	Val	Glu	Arg	Tyr
					130			135			140				
Val	Ala	Ile	Leu	His	Pro	Phe	Arg	Ala	Lys	Leu	Gln	Ser	Thr	Arg	Arg
					145			150			155			160	

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Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe  
165 170 175

Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro  
180 185 190

Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro  
195 200 205

Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr  
210 215 220

Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu  
225 230 235 240

Arg Val Ser Ile Ala Gly Val Ala Gly  
245

<210> 19

<211> 222

<212> DNA

<213> H.Sapiens

<400> 19

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attgtctatg catttatgaa tgaaaacttc aaaaaaaaaatg ttttgcgtgc agtttgttat 120

tgcatacgatataaaaacccttt ctctccagca caaaggcatg gaaattcagg aattacaatg 180

atgcggaaga aagcaaagttt ttccctcaga gagaatccag tg 222

<210> 20

<211> 73

<212> PRT

<213> H.Sapiens

<400> 20

Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile Gly Phe Ser Asn Ser  
1 5 10 15

Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn Glu Asn Phe Lys Lys  
20 25 30

Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val Asn Lys Thr Phe Ser  
35 40 45

Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr Met Met Arg Lys Lys  
50 55 60

Ala Lys Phe Ser Leu Arg Glu Asn Pro  
65 70

<210> 21

<211> 447

<212> DNA

<213> H.Sapiens

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1 . 5 10 15

Leu Arg Leu Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser  
20 25 30

Gly Ser Gln Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg  
35 40 45

Arg Cys Leu Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg  
50 55 60

Ser Ser Pro Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser  
65 70 75 80

Pro Gly

<210> 27  
<211> 420  
<212> DNA  
<213> H.Sapiens

<220>  
<221> misc\_feature  
<222> (81)..(106)  
<223> n is any nucleic acid

<400> 27  
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tcgcgggtcc gcagcctcct nnnnnnnnnn nnnnnnnnnn nnnnnntggc agagcttgcg 120  
cgcgatgcgg gcgtacatga ccacgatgag cgccagcggc gccaggtaga tgtgcgagaa 180  
gagcacagtg gtgttagaccc tgcgcatgcc cttctcggc caggcctccc agcaggagta 240  
gagaggtag gagcggttgc gggcgtccac catgaagtgg tgctcctcac gggtgacggt 300  
cagcgtgacg gccgagggac acatgatgag cagcgccagg gcccagatga cggcgatggt 360  
gacgagcgcc ttccgcaggg tcagttctc gcggaaaggg tgcacgatgc agcggAACCT 420

<210> 28  
<211> 139  
<212> PRT  
<213> H.Sapiens

<220>  
<221> UNSURE  
<222> (104)..(113)  
<223> Xaa is Unknown

<400> 28

Phe Arg Cys Ile Val His Pro Phe Arg Glu Lys Leu Thr Leu Arg Lys  
1 5 10 15

Ala Leu Val Thr Ile Ala Val Ile Trp Ala Leu Ala Leu Leu Ile Met  
 20 25 30

Cys Pro Ser Ala Val Thr Leu Thr Val Thr Arg Glu Glu His His Phe  
 35 40 45

Met Val Asp Ala Arg Asn Arg Ser Tyr Pro Leu Tyr Ser Cys Trp Glu  
 50 55 60

Ala Trp Pro Glu Lys Gly Met Arg Arg Val Tyr Thr Thr Val Leu Phe  
 65 70 75 80

Ser His Ile Tyr Leu Ala Pro Leu Ala Leu Ile Val Val Met Tyr Ala  
 85 90 95

Arg Ile Ala Arg Lys Leu Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 100 105 110

Xaa Glu Ala Ala Asp Pro Arg Ala Ser Arg Arg Arg Ala Arg Val Val  
 115 120 125

His Met Leu Val Met Val Ala Leu Phe Phe Thr  
 130 135

<210> 29  
 <211> 318  
 <212> DNA  
 <213> H.Sapiens

<400> 29  
 gcagggggcg tgagtccctca ggcacttctt gaggtccttg ttgagcagga agcagacaat 60  
 tgggttgacg gcagcctggg cgaagctcat ccaaacagca gtggccaggt agcggtgggg 120  
 cacagcacag gcttcacaa acactcgcca gtagcaggcc acgatgtagg gtgaccagag 180  
 gagcagaaaag agcagtgtga tcgcgtagaa catgcggccc agctgcttt cacccttgcac 240  
 ctcgtccatg cccagtagcc gccggctggc tgcattccca ttctgcccga tacccagcag 300  
 gtttggtggc atgggccc 318

<210> 30  
 <211> 106  
 <212> PRT  
 <213> H.Sapiens

<400> 30

Gly Pro Met Pro Pro Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala  
 1 5 10 15

Ala Ser Arg Arg Leu Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln  
 20 25 30

Leu Gly Arg Met Phe Tyr Ala Ile Thr Leu Leu Phe Leu Leu Trp  
 35 40 45

Ser Pro Tyr Ile Val Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys  
 50 55 60

Ala Val Pro His Arg Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala  
 65 70 75 80

Gln Ala Ala Val Asn Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu  
 85 90 95

Lys Lys Cys Leu Arg Thr His Ala Pro Cys  
 100 105

<210> 31  
 <211> 354  
 <212> DNA  
 <213> H.Sapiens

<400> 31  
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 cattgtgaaa gcccattcggt tgggtgtattt ccacttcatt ttaaaaaggat gcacaagtcc 120  
 ctgggtgcctt tccacagcaa tgcaggtcat agtgaggatt tctgtcacaa cagcggtaga 180  
 ctggacaaat ggcaccatct tgcaaatgaa agcacctgca gtaaggaaat aggataaatac 240  
 atacatcaaa acaaaaagaa taaaggtttc atctgtgtct ttgttaattat cactatcagt 300  
 ccattctgag cctctgccaa aaagtttgat aattgttaatt actctgtaga caca 354

<210> 32  
 <211> 117  
 <212> PRT  
 <213> H.Sapiens

<400> 32

Val Tyr Arg Val Ile Thr Ile Ile Lys Leu Phe Gly Arg Gly Ser Glu  
 1 5 10 15

Trp Thr Asp Ser Asp Asn Tyr Lys Asp Thr Asp Glu Thr Phe Ile Leu  
 20 25 30

Phe Val Leu Met Tyr Asp Leu Ser Tyr Phe Leu Thr Ala Gly Ala Phe  
 35 40 45

Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala Val Val Thr Glu  
 50 55 60

Ile Leu Thr Met Thr Cys Ile Ala Val Glu Arg His Gln Gly Leu Val  
 65 70 75 80

His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg Arg Ala Phe Thr  
 85 90 95

Met Leu Gly Glu Ala Thr Gly Cys Ala Asn Gly Ser Val Asn Asp Ile  
 100 105 110

Leu His Tyr Arg Ile  
115

<210> 33

<211> 621

<212> DNA

<213> H.Sapiens

<400> 33

gagcaacatg atcttttga agtacttgac ggtgtcggttc ttgacggtca cgaagcacag 60  
agtgttgatc atgctgttgc tcatggcgat gcactcgacg atgtagaagg cagttaggta 120  
gtgcttctcc ttcacaaaca cggtgggaa gaagtcgcgc acgatggtga agccgtagaa 180  
ggcgccccag catagcacgt aggcggtgag gatgcacatg agcaccagga ccgtttcct 240  
gcggcagcgc agcctttgc ggatctgctc tgtctggaat ccagggaccg cttgaacca 300  
gagctcccgagatccctgg catagcacag ggtcatggtg accacgggacccac 360  
tatgccaaag ataaagagga agtaggactt gtagtagagc tgctggtcca caggccagat 420  
ctggccgcag aagatctttt cctggctttt gacaatgacg aggaccgtct cggtggtgaa 480  
gtaggcggaa gggatggcga tcaggatgga caccgtccac accaaggcaa tcaggccagt 540  
ggctgtttgg cacttcattt gtggtctcag cggatggaca atagccagat acctaggca 600  
agaacacaag tggaggcagc c 621

<210> 34

<211> 207

<212> PRT

<213> H.Sapiens

<400> 34

Gly Cys Leu His Leu,Cys Ser Cys Pro Arg Tyr Leu Ala Ile Val His  
1 5 10 15

Pro Leu Arg Pro Arg Met Lys Cys Gln Thr Ala Thr Gly Leu Ile Ala  
20 25 30

Leu Val Trp Thr Val Ser Ile Leu Ile Ala Ile Pro Ser Ala Tyr Phe  
35 40 45

Thr Thr Glu Thr Val Leu Val Ile Val Lys Ser Gln Glu Lys Ile Phe  
50 55 60

Cys Gly Gln Ile Trp Pro Val Asp Gln Gln Leu Tyr Tyr Lys Ser Tyr  
65 70 75 80

Phe Leu Phe Ile Phe Gly Ile Glu Phe Val Gly Pro Val Val Thr Met  
85 90 95

Thr Leu Cys Tyr Ala Arg Ile Ser Arg Glu Leu Trp Phe Lys Ala Val

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100 105 110

Pro Gly Phe Gln Thr Glu Gln Ile Arg Lys Arg Leu Arg Cys Arg Arg  
115 120 125

Lys Thr Val Leu Val Leu Met Cys Ile Leu Thr Ala Tyr Val Leu Cys  
130 135 140

Trp Ala Pro Phe Tyr Gly Phe Thr Ile Val Arg Asp Phe Phe Pro Thr  
145 150 155 160

Val Phe Val Lys Glu Lys His Tyr Leu Thr Ala Phe Tyr Ile Val Glu  
165 170 175

Cys Ile Ala Met Ser Asn Ser Met Ile Asn Thr Leu Cys Phe Val Thr  
180 185 190

Val Lys Asn Asp Thr Val Lys Tyr Phe Lys Lys Ile Met Leu Leu  
195 200 205

<210> 35

<211> 483

<212> DNA

<213> H.Sapiens

<400> 35

cagccacact gcagtgtatga aatcaaatgt ccaacaccaa ccatagtcac cattactaac 60

taagaagcca caaaaacttcc cttccagggt gttcagcagc agggacaggg cccagggcag 120

ggcacacatg acagttgaca ggtttcttgg gcagcagcag cagtaccaga taggccgcag 180

gacagacagg cagcactcag tactgtatggc actcagcatg ctcaggccta caaggtaggc 240

aaaggtcatc acgctggtga agaagctagg gaaattgatg gagatggaac agaagaagtt 300

actgaggtac accaggcaat ttataatctg gaagcagagg aagaggaagt cggcccccgc 360

caggctgagg acgttagacag agaaggcggt cctgcgcatt cggaaagccca ggagccagag 420

cacaaacccg tttcctacca gcccgaccag ggcaatgaaa aggatcagga agaccggat 480

cag 483

<210> 36

<211> 161

<212> PRT

<213> H.Sapiens

<400> 36

Leu Ile Pro Val Phe Leu Ile Leu Phe Ile Ala Leu Val Gly Leu Val  
1 5 10 15

Gly Asn Gly Phe Val Leu Trp Leu Leu Gly Phe Arg Met Arg Arg Asn  
20 25 30

Ala Phe Ser Val Tyr Val Leu Ser Leu Ala Gly Ala Asp Phe Leu Phe

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35

40

45

Leu Cys Phe Gln Ile Ile Asn Cys Leu Val Tyr Leu Ser Asn Phe Phe  
50 55 60

Cys Ser Ile Ser Ile Asn Phe Pro Ser Phe Phe Thr Ser Val Met Thr  
65 70 75 80

Phe Ala Tyr Leu Val Gly Leu Ser Met Leu Ser Ala Ile Ser Thr Glu  
85 90 95

Cys Cys Leu Ser Val Leu Arg Pro Ile Trp Tyr Cys Cys Cys Cys Pro  
100 105 110

Arg Asn Leu Ser Thr Val Met Cys Ala Leu Pro Trp Ala Leu Ser Leu  
115 120 125

Leu Leu Asn Thr Leu Glu Gly Lys Phe Cys Gly Phe Leu Val Ser Asn  
130 135 140

Gly Asp Tyr Gly Trp Cys Trp Thr Phe Asp Phe Ile Thr Ala Val Trp  
145 150 155 160

Leu

<210> 37

<211> 330

<212> DNA

<213> H.Sapiens

<400> 37

gagagtctga ttctgactta catcacatat gtaggcctgg gcatttctat ttgcagcctg 60

atcccttgct tgtccgttga ggtcctagtc tggagccaag tgacaaaagac agagatcacc 120

tatttacgcc atgtgtgcat tgttaacatt gcagccactt tgctgatggc agatgtgtgg 180

ttcatttgtgg cttcccttct tagtggccca ataacacacc acaaggatg tgtggcagcc 240

acattttttg gtcatttcgtt ttaccttct gtattttct ggatgcttgc caaggcactc 300

cttatcctct atggaatcat gattgttttc 330

<210> 38

<211> 110

<212> PRT

<213> H.Sapiens

<400> 38

Glu Ser Leu Ile Leu Thr Tyr Ile Thr Tyr Val Gly Leu Gly Ile Ser  
1 5 10 15

Ile Cys Ser Leu Ile Leu Cys Leu Ser Val Glu Val Leu Val Trp Ser  
20 25 30

Gln Val Thr Lys Thr Glu Ile Thr Tyr Leu Arg His Val Cys Ile Val

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35

40

45

Asn Ile Ala Ala Thr Leu Leu Met Ala Asp Val Trp Phe Ile Val Ala  
50 55 60

Ser Phe Leu Ser Gly Pro Ile Thr His His Lys Gly Cys Val Ala Ala  
65 70 75 80

Thr Phe Phe Gly His Phe Phe Tyr Leu Ser Val Phe Phe Trp Met Leu  
85 90 95

Ala Lys Ala Leu Leu Ile Leu Tyr Gly Ile Met Ile Val Phe  
100 105 110

<210> 39

<211> 628

<212> DNA

<213> H.Sapiens

<400> 39

ttgtgtggca gtagagagat gtcaggcttc agagtcaaca agaactggat ttcaaactgg 60

atttgaggac ccccacccctt ggtaagtgc ttattatctg cgagcctctg tttctctctt 120

ctttaaatga ggacagtaaa tcccatacgg cagggtggtg gggagaatca gagatgatac 180

agctggtgat cacatctggt ttgtgttccc aggggcacca gactagggtt tctgagcatg 240

gatccaaccg tcccagtctt cggcacaaaa ctgacaccaa tcaacggacg tgaggagact 300

ccttgctaca atcagaccct gagttcacg gtgctgacgt gcatcatttc cttgtcgga 360

ctgacaggaa acgcggtagt gctctggctc ctgggctacc gcatgcgcag gaacgctgtc 420

tccatctaca tcctcaacct ggccgcagca gacttcctct tcctcagctt ccagattata 480

cgttcgccat tacgcctcat caatatcagc catctcatcc gcaaaatcct cgtttctgtg 540

atgaccttac cctactttac aggcttgagt atgctgagcg ccatcagcac cgagcgctgc 600

ctgtctgttc tgtggccat ctggtaacc 628

<210> 40

<211> 205

<212> PRT

<213> H.Sapiens

<400> 40

Leu Cys Gly Ser Arg Glu Met Ser Gly Phe Arg Val Asn Lys Asn Trp  
1 5 10 15

Ile Ser Asn Trp Ile Gly Pro Pro Pro Leu Val Ser Asp Leu Leu Ser  
20 25 30

Ala Ser Leu Cys Phe Ser Leu Leu Met Arg Thr Val Asn Pro Ile Arg  
35 40 45

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Gln Gly Gly Gly Glu Asn Gln Arg Tyr Ser Trp Ser His Leu Val Cys  
50 55 60

Val Pro Arg Gly Thr Arg Leu Gly Phe Leu Ser Met Asp Pro Thr Val  
65 70 75 80

Pro Val Phe Gly Thr Lys Leu Thr Pro Ile Asn Gly Arg Glu Glu Thr  
85 90 95

Pro Cys Tyr Asn Gln Thr Leu Ser Phe Thr Val Leu Thr Cys Ile Ile  
100 105 110

Ser Leu Val Gly Leu Thr Gly Asn Ala Val Val Leu Trp Leu Leu Gly  
115 120 125

Tyr Arg Met Arg Arg Asn Ala Val Ser Ile Tyr Ile Leu Asn Leu Ala  
130 135 140

Ala Ala Asp Phe Leu Phe Leu Ser Phe Gln Ile Ile Arg Ser Pro Leu  
145 150 155 160

Arg Leu Ile Asn Ile Ser His Leu Ile Arg Lys Ile Leu Val Ser Val  
165 170 175

Met Thr Phe Pro Tyr Phe Thr Gly Leu Ser Met Leu Ser Ala Ile Ser  
180 185 190

Thr Glu Arg Cys Leu Ser Val Leu Trp Pro Ile Trp Tyr  
195 200 205

<210> 41

<211> 319

<212> DNA

<213> H.Sapiens

<400> 41

acagaaaagca aggccaccag gaccttaggc atagtcatgg gagtgtttgt gttgtgctgg 60

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ctgtacaatg tcttcctctg gctaggctat ttcaactctg ctttcaatcc cattttatat 180

ggcatgcttt atccttggtt tcgcaaggca ttgaggatga ttgtcacagg catgatcttc 240

caccctgact cttccaccct aagcctgttt tctgccccatg cttaggctgt gttcatcatt 300

caataggact cttttctgg 319

<210> 42

<211> 103

<212> PRT

<213> H.Sapiens

<400> 42

Thr Glu Ser Lys Ala Thr Arg Thr Leu Gly Ile Val Met Gly Val Phe  
1 5 10 15

## 00431PHRM293.ST25

Val Leu Cys Trp Leu Pro Phe Phe Val Leu Thr Ile Thr Asp Pro Phe  
 20 25 30

Ile Asn Phe Thr Thr Leu Glu Asp Leu Tyr Asn Val Phe Leu Trp Leu  
 35 40 45

Gly Tyr Phe Asn Ser Ala Phe Asn Pro Ile Leu Tyr Gly Met Leu Tyr  
 50 55 60

Pro Trp Phe Arg Lys Ala Leu Arg Met Ile Val Thr Gly Met Ile Phe  
 65 70 75 80

His Pro Asp Ser Ser Thr Leu Ser Leu Phe Ser Ala His Ala Ala Val  
 85 90 95

Phe Ile Ile Gln Asp Ser Phe  
 100

<210> 43

<211> 515

<212> DNA

<213> H.Sapiens

<400> 43

taggaatctc agagaagaaa gtaaggaacc agaaaaccat aaaagaatgt aaatggaaaa 60

gaatcagcaa atcttattca cttatcacta aatctaaaat atgtcaaaat acatgaagac 120

aacaaatgct ttagaacaac tggtaatgt attgtcctac aacttggcat atgatcatgc 180

ttgcctctct atgtccaaat gtttattttt gcagttgacc ttaatttcaa gttagtttg 240

aggtctctac agtaatgttt ttaatctgtc tctacttctt cagaaaataa attagttgtt 300

gacgaatcag tccttaagac cttgccgctt acaataagtt ttattgcctt cccaaaccat 360

tggtaaaaga aagcataaat caaggggttc atagctgaat tataataaac acaccaaact 420

aaaatctcat aaacataagg aggagttata aaattcatat aagcatcaat cactgcatca 480

acgaggtatg gtagccaaga gacaagaaat gctgc 515

<210> 44

<211> 148

<212> PRT

<213> H.Sapiens

<400> 44

Leu His Gln Arg Gly Met Val Ala Lys Arg Gln Glu Met Leu Ala Ala  
 1 5 10 15

Phe Leu Val Ser Trp Leu Pro Tyr Leu Val Asp Ala Val Ile Asp Ala  
 20 25 30

Tyr Met Asn Phe Ile Thr Pro Pro Tyr Val Tyr Glu Ile Leu Val Trp  
 35 40 45

## 00431PHRM293.ST25

Cys Val Tyr Tyr Asn Ser Ala Met Asn Pro Leu Ile Tyr Ala Phe Phe  
 50 55 60

Tyr Gln Trp Phe Gly Lys Ala Ile Lys Leu Ile Val Ser Gly Lys Val  
 65 70 75 80

Leu Arg Thr Asp Ser Ser Thr Thr Asn Leu Phe Ser Glu Glu Val Glu  
 85 90 95

Thr Asp Lys His Tyr Cys Arg Asp Leu Lys Thr Asn Leu Lys Leu Arg  
 100 105 110

Ser Thr Ala Lys Ile Asn Thr Trp Thr Arg Gly Lys His Asp His Met  
 115 120 125

Pro Ser Cys Arg Thr Ile His Ser Thr Val Val Leu Lys His Leu Leu  
 130 135 140

Ser Ser Cys Ile  
 145

<210> 45

<211> 726

<212> DNA

<213> H.Sapiens

<400> 45

ctggaaagag gtcctcgatc tatcctctac gccgtccttg gttttggggc tgtgctggca 60

gcgtttggaa acttactggt catgattgct atccttcaact tctaacaact gcacacaccc 120

acaaaactttc tgattgcgtc gctggcctgt gctgacttct tggtgggagt cactgtgatg 180

cccttcagca cagttaggtc tgtggagagc tggggactact ttggggacag ttactgtaaa 240

ttccatacat gtttgacac atctttctgt tttgcttctt tatttcattt atgctgtatc 300

tctgttgata gatacattgc tggactgtat cctctgacct atccaaccaa gtttactgtg 360

tcagtttcag ggatatgcat tggctttcc tggtttttt ctgtcacata cagctttcg 420

atctttaca cgggagccaa cgaagaagga attgaggaat tagtagttgc tctaacctgt 480

gtaggaggct gccaggctcc actgaatcaa aactgggtcc tactttgttt tcttctattc 540

tttataccca atgtgccat ggtgtttata tacagtaaga tattttgggt ggccaagcat 600

caggctagga agatagaaag tacagccagc caagctcagt ccttctcaga gagttacaag 660

gaaagagtag caaaaagaga gagaaaggct gccaaaacct tggaaattgc tatggcagca 720

tttctt 726

<210> 46

<211> 241

<212> PRT

<213> H.Sapiens

&lt;400&gt; 46

Leu Glu Arg Gly Pro Arg Ser Ile Leu Tyr Ala Val Leu Gly Phe Gly  
 1 5 10 15

Ala Val Leu Ala Ala Phe Gly Asn Leu Leu Val Met Ile Ala Ile Leu  
 20 25 30

His Phe Gln Leu His Thr Pro Thr Asn Phe Leu Ile Ala Ser Leu Ala  
 35 40 45

Cys Ala Asp Phe Leu Val Gly Val Thr Val Met Pro Phe Ser Thr Val  
 50 55 60

Arg Ser Val Glu Ser Cys Trp Tyr Phe Gly Asp Ser Tyr Cys Lys Phe  
 65 70 75 80

His Thr Cys Phe Asp Thr Ser Phe Cys Phe Ala Ser Leu Phe His Leu  
 85 90 95

Cys Cys Ile Ser Val Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Thr  
 100 105 110

Tyr Pro Thr Lys Phe Thr Val Ser Val Ser Gly Ile Cys Ile Val Leu  
 115 120 125

Ser Trp Phe Phe Ser Val Thr Tyr Ser Phe Ser Ile Phe Tyr Thr Gly  
 130 135 140

Ala Asn Glu Glu Gly Ile Glu Glu Leu Val Val Ala Leu Thr Cys Val  
 145 150 155 160

Gly Gly Cys Gln Ala Pro Leu Asn Gln Asn Trp Val Leu Leu Cys Phe  
 165 170 175

Leu Leu Phe Phe Ile Pro Asn Val Ala Met Val Phe Ile Tyr Ser Lys  
 180 185 190

Ile Phe Leu Val Ala Lys His Gln Ala Arg Lys Ile Glu Ser Thr Ala  
 195 200 205

Ser Gln Ala Gln Ser Phe Ser Glu Ser Tyr Lys Glu Arg Val Ala Lys  
 210 215 220

Arg Glu Arg Lys Ala Ala Lys Thr Leu Gly Ile Ala Met Ala Ala Phe  
 225 230 235 240

Leu

<210> 47  
 <211> 660  
 <212> DNA  
 <213> H.Sapiens

<400> 47  
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 ctcaatccag ttctctatgt cttcattggg catgacttct gggagcactt gctccactcc 120

ctgctagctg	ccttagaacg	ggcacttagc	gaggagccag	atagtgcctg	aatcccagct	180
cccaggcaga	tgagtcctt	ataacatgac	ccaatttcct	actccatttt	cccaccactc	240
aatcctcttc	ccaaacagct	ctaccataat	ccaacatcca	acagaattta	agagaataaa	300
ccacaacttt	taagtgagct	ctatgtgcta	ggtcatgttt	tagaatacaa	ccttaagtgc	360
ctggaagatg	gaggcaagaa	acaaacaagg	tctcattctt	tagaggaaga	cagttcacca	420
agactcaaac	agaaaaaaag	atagttatct	tgtgacaaaaa	caagtcataa	aattgggtca	480
ggacctgcag	caatgacttt	atgctagaat	ccagagcact	agcagggaaac	tgcttaaatt	540
ttacttaatc	aaagtcaagt	ttggacatac	atgtcaggtt	aaacctagca	gagatgagct	600
accttgattt	taaaaacttca	agggatagct	caatgtcatc	aagatccttt	tgatgacttg	660

<210> 48  
 <211> 211  
 <212> PRT  
 <213> H.Sapiens

<400> 48

Asn	Gln	Val	Ala	Leu	Leu	Leu	Arg	Pro	Leu	Ala	Leu	Ser	Met	Ala	Phe
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Ile	Asn	Ser	Cys	Leu	Asn	Pro	Val	Leu	Tyr	Val	Phe	Ile	Gly	His	Asp
							20		25			30			
Phe	Trp	Glu	His	Leu	Leu	His	Ser	Leu	Leu	Ala	Ala	Leu	Glu	Arg	Ala
							35		40			45			
Leu	Ser	Glu	Glu	Pro	Asp	Ser	Ala	Ile	Pro	Ala	Pro	Arg	Gln	Met	Ser
					50				55			60			
Pro	Leu	His	Asp	Pro	Ile	Ser	Tyr	Ser	Ile	Phe	Pro	Pro	Leu	Asn	Pro
					65				70			75		80	
Leu	Pro	Lys	Gln	Leu	Tyr	His	Asn	Pro	Thr	Ser	Asn	Arg	Ile	Glu	Asn
							85		90			95			
Lys	Pro	Gln	Leu	Leu	Ser	Glu	Leu	Tyr	Val	Leu	Gly	His	Val	Leu	Glu
							100		105			110			
Tyr	Asn	Leu	Lys	Cys	Leu	Glu	Asp	Gly	Gly	Lys	Lys	Gln	Thr	Arg	Ser
							115		120			125			
His	Ser	Leu	Glu	Glu	Asp	Ser	Ser	Pro	Arg	Leu	Lys	Gln	Lys	Lys	Arg
							130		135			140			
Leu	Ser	Cys	Asp	Lys	Thr	Ser	His	Lys	Ile	Gly	Ser	Gly	Pro	Ala	Ala
							145		150			155		160	
Met	Thr	Leu	Cys	Asn	Pro	Glu	His	Gln	Glu	Thr	Ala	Ile	Leu	Leu	Asn
							165		170			175			

## 00431PHRM293.ST25

Gln Ser Gln Val Trp Thr Tyr Met Ser Gly Lys Thr Gln Arg Ala Thr  
 180 185 190

Leu Ile Leu Lys Leu Gln Gly Ile Ala Gln Cys His Gln Asp Pro Phe  
 195 200 205

Asp Asp Leu  
 210

<210> 49  
 <211> 465  
 <212> DNA  
 <213> H.Sapiens

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 agcggaggcg cgccgtgggc ctggccgccc tggcttgct ggccttgtc acctgcttcg 120  
 cccccaacaa cttcgtgctc ctggcgacaca tcgtgagccg cctgttctac ggcaagagct 180  
 actaccacgt gtacaagctc acgctgtgtc tcagctgcct caacaactgt ctggaccctg 240  
 ttgtttatta ctttgcgtcc cggaaattcc agctgcgcct gcggaaatat ttgggctgcc 300  
 gccgggtgcc cagagacacc ctggacacgc gccgcgagag cctcttctcc gccaggacca 360  
 cgtccgtgcg ctccgaggcc ggtgcgcacc ctgaaggat ggagggagcc accaggcccg 420  
 gcctccagag gcaggagagt gtgttctgag tcccgggggc gcagc 465

<210> 50  
 <211> 160  
 <212> PRT  
 <213> H.Sapiens

<400> 50

Leu Phe Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu Glu Ala His  
 1 5 10 15

Gly Arg Glu Gln Arg Arg Ala Val Gly Leu Ala Ala Val Val Leu  
 20 25 30

Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val Leu Leu Ala  
 35 40 45

His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr His Val Tyr  
 50 55 60

Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu Asp Pro Phe  
 65 70 75 80

Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu Arg Glu Tyr  
 85 90 95

Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr Arg Arg Glu

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100 105 110

Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu Ala Gly Ala  
115 120 125

His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu Gln Arg Gln  
130 135 140

Glu Ser Val Phe Val Pro Gly Ala Gln Ala Ala Pro Pro Gly Leu Arg  
145 150 155 160

<210> 51  
<211> 603  
<212> DNA  
<213> H.Sapiens

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ccggaaccca cagggccccg tgggccatga gaggctcctg gacttgaacc tcaggacact 120  
cccactctgg ctgcccggcag gcatggaaagc tggatgagca ggcaggagct ggcagtgggg  
gtggagagcc ataggctatt ggggtggaca ggcttgggtg cctcatggga gctcccccattg 180  
ggagctgtgg ccccttgggg cctcttattt ctcacccag gcttcccgag gagaggttca 360  
agtcagaaga tgccccaaag atccacgtgg ccctgggtgg cagcctgttc ctcctgaatc  
tggccttctt ggtcaatgtg gggagtggtct caaagggttc tggatgtgtcc tggatggccc 420  
ggggggctgt cttccactac ttccctgtct gtgccttcac ctggatgggc cttgaagcct 540  
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agc 600  
603

<210> 52  
<211> 198  
<212> PRT  
<213> H.Sapiens

<400> 52

Glu Thr Tyr Ser Ala Leu Tyr Pro Thr Phe Asn Ser Leu Cys Tyr Ser  
1 5 10 15

Pro Ala Ser Phe Ser Gly Leu Ile Phe Pro Ile Ile Leu Pro His Ile  
20 25 30

Asp Gln Gly Met Arg Leu Ala Gly Ser Gly Thr His Arg Ala Pro Trp  
35 40 45

Ala Met Arg Gly Ser Trp Thr Thr Ser Gly His Ser His Ser Gly Cys  
50 55 60

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Arg Gln Gly Trp Lys Leu Asp Glu Gln Ala Gly Ala Gly Ser Gly Gly  
 65 70 75 80

Gly Glu Pro Ala Ile Gly Val Asp Arg Leu Gly Cys Leu Met Gly Ala  
 85 90 95

Pro His Gly Ser Cys Gly Pro Leu Gly Pro Leu Ile Ser His Pro Arg  
 100 105 110

Leu Ser Arg Glu Arg Phe Lys Ser Glu Asp Ala Pro Lys Ile His Val  
 115 120 125

Ala Leu Gly Gly Ser Leu Phe Leu Leu Asn Leu Ala Phe Leu Val Asn  
 130 135 140

Val Gly Ser Gly Ser Lys Gly Ser Asp Ala Ala Cys Trp Ala Arg Gly  
 145 150 155 160

Ala Val Phe His Tyr Phe Leu Leu Cys Ala Phe Thr Trp Met Gly Leu  
 165 170 175

Glu Ala Phe His Leu Tyr Leu Leu Ala Val Arg Val Phe Asn Thr Tyr  
 180 185 190

Phe Gly His Tyr Phe Leu  
 195

<210> 53  
 <211> 335  
 <212> DNA  
 <213> H.Sapiens

<400> 53  
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 caaacacagc cagcacagcc ccaaagccaa acactatgta cagaatcacc cgggatcccg  
 gcgagaaggg gatttcaca caggaccat tcacgttcgc gtagcacagc tgcacagcca 120  
 ccagcaggga tgaattgctg ctcataacgc tggattttac atatggagaa attttgtcct  
 tgttgattat cacaaaaat acaggattgt tcctgatttt cattgctcct gcggaaaaaa 180  
 acacatattc accaggatgc cagaggaat gatca 240  
 300  
 335

<210> 54  
 <211> 111  
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<400> 54

Asp His Phe Leu Trp His Pro Gly Glu Tyr Val Phe Phe Ser Ala Gly  
 1 5 10 15

Ala Met Lys Ile Arg Asn Asn Pro Val Phe Phe Val Ile Ile Asn Lys  
 20 25 30

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Asp Lys Ile Ser Pro Tyr Val Asn Thr Ser Val Met Ser Ser Asn Ser  
35 40 45

Ser Leu Leu Val Ala Val Gln Leu Cys Tyr Ala Asn Val Asn Gly Ser  
50 55 60

Cys Val Lys Ile Pro Phe Ser Pro Gly Ser Arg Val Ile Leu Tyr Ile  
65 70 75 80

Val Phe Gly Phe Gly Ala Val Leu Ala Val Phe Gly Asn Leu Leu Val  
85 90 95

Met Ile Ser Ile Leu His Phe Lys Gln Leu His Ser Pro Thr Asn  
100 105 110

<210> 55

<211> 586

<212> DNA

<213> H.Sapiens

<400> 55

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ctattcattc atagtcttac ttgattttta aaaactcatt tcgcttggtt atttaaagg 120

tatcctgaac ttcgtctatc caactgctta tataatgttca gaaaacaaat tcatgggtgc 180

tgaactgttc tttaaaacctt gaccagttac aataactttt attgctttcc taaaccatgg 240

gtaaaaataaa gcataaatca aaggattcat ggctgagttt taataagcac accaacagca 300

tcataaatac aggcagggtt tataaagccc ataaaggcat caattaatga atcaatgcta 360

tatggtaacc atgaaatcat aaatgctacc actgtgaccc ccagggtttt agctgcttt 420

ctctctctcc tggccactct ggctttgtta ctctctgagg atgattctgt cttgctacca 480

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atcataataa aggttaggtat aaagaaggat agaaaatctg tcaaca 586

<210> 56

<211> 190

<212> PRT

<213> H.Sapiens

<400> 56

Leu Thr Asp Phe Leu Ser Phe Phe Ile Pro Thr Phe Ile Met Ile Ile  
1 5 10 15

Leu Tyr Gly Asn Ile Phe Leu Val Ala Arg Arg Gln Ala Lys Lys Ile  
20 25 30

Glu Asn Thr Gly Ser Lys Thr Glu Ser Ser Ser Glu Ser Tyr Lys Ala  
35 40 45

Arg Val Ala Arg Arg Glu Arg Lys Ala Ala Lys Thr Leu Gly Val Thr

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50

55

60

Val Val Ala Phe Met Ile Ser Trp Leu Pro Tyr Ser Ile Asp Ser Leu  
 65 70 75 80

Ile Asp Ala Phe Met Gly Phe Ile Thr Pro Ala Cys Ile Tyr Glu Ile  
 85 90 95

Cys Cys Trp Cys Ala Tyr Tyr Asn Ser Ala Met Asn Pro Leu Ile Tyr  
 100 105 110

Ala Leu Phe Tyr Pro Trp Phe Arg Lys Ala Ile Lys Val Ile Val Thr  
 115 120 125

Gly Gln Val Leu Lys Asn Ser Ser Ala Thr Met Asn Leu Phe Ser Glu  
 130 135 140

His Ile Ala Val Gly Thr Lys Phe Arg Ile Pro Leu Lys Leu Pro Ser  
 145 150 155 160

Glu Met Ser Phe Lys Ser Ser Lys Thr Met Asn Glu Gln Ile Asn Cys  
 165 170 175

Ser Ser Asn Lys Gln Ile Asn Val Phe Gln Ser Cys Asp Val  
 180 185 190

<210> 57

<211> 976

<212> DNA

<213> H.Sapiens

<400> 57

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ctgtctacgt cctcagcctg gccggggccg acttccttctt cctctgcttc cagattataa	180
attgcctgggt gtacctcagt aacttcttctt gttccatctc catcaatttc cctagttct	240
tcaccactgt gatgacctgt gcctaccttg caggcctgag catgctgagc accgtcagca	300
ccgagcgctg cctgtccgtc ctgtggccca tctggatcg ctggccgc cccagacacc	360
tgtcagcggt cgtgtgtgtc ctgctctggg ccctgtccct actgctgagc atcttggaaag	420
ggaagttctg tggcttctta ttttagtgatg gtgactctgg ttgggtgtcaag acatttgatt	480
tcatcaactgc agcgtggctg attttttat tcatggttct ctgtgggtcc agtctggccc	540
tgctggtcag gatcctctgt ggctccaggg gtctgccact gaccaggctg tacctgacca	600
tcctgctcac agtgctggtg tccctcctct gcggcctgcc ctttggcatt cagtgggtcc	660
taatattatg gatctgaaag gattctgatg tcttattttg tcatattcat ccagttcag	720
ttgtcctgtc atctcttaac agcagtgccca accccatcat ttacttcttc gtgggtcttt	780
tttaggaagca gtggcggttg cagcacccga tcctcaagct ggctctccag agggctctgc	840

aggacattgc tgaggtggat cacagtgaag gatgcttccg tcagggcacc cggagattca 900  
 aagaagcatt ctggtgttagg gatggacccc tctacttcca tcatatatat gtggcttga 960  
 gaggcaactt tgcccc 976

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 <211> 324  
 <212> PRT  
 <213> H.Sapiens

<220>  
 <221> UNSURE  
 <222> (266)..(266)  
 <223> Xaa is Unknown

<400> 58

Cys Gly Lys Glu Thr Leu Ile Pro Val Phe Leu Ile Leu Phe Ile Ala  
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 Leu Val Gly Leu Val Gly Asn Gly Phe Val Leu Trp Leu Leu Gly Phe  
 20 25 30  
 Arg Met Arg Arg Asn Ala Phe Ser Val Tyr Val Leu Ser Leu Ala Gly  
 35 40 45  
 Ala Asp Phe Leu Phe Leu Cys Phe Gln Ile Ile Asn Cys Leu Val Tyr  
 50 55 60  
 Leu Ser Asn Phe Phe Cys Ser Ile Ser Ile Asn Phe Pro Ser Phe Phe  
 65 70 75 80  
 Thr Thr Val Met Thr Cys Ala Tyr Leu Ala Gly Leu Ser Met Leu Ser  
 85 90 95  
 Thr Val Ser Thr Glu Arg Cys Leu Ser Val Leu Trp Pro Ile Trp Tyr  
 100 105 110  
 Arg Cys Arg Arg Pro Arg His Leu Ser Ala Val Val Cys Val Leu Leu  
 115 120 125  
 Trp Ala Leu Ser Leu Leu Leu Ser Ile Leu Glu Gly Lys Phe Cys Gly  
 130 135 140  
 Phe Leu Phe Ser Asp Gly Asp Ser Gly Trp Cys Gln Thr Phe Asp Phe  
 145 150 155 160  
 Ile Thr Ala Ala Trp Leu Ile Phe Leu Phe Met Val Leu Cys Gly Ser  
 165 170 175  
 Ser Leu Ala Leu Leu Val Arg Ile Leu Cys Gly Ser Arg Gly Leu Pro  
 180 185 190  
 Leu Thr Arg Leu Tyr Leu Thr Ile Leu Leu Thr Val Leu Val Ser Leu  
 195 200 205

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Leu Cys Gly Leu Pro Phe Gly Ile Gln Trp Phe Leu Ile Leu Trp Ile  
 210 215 220

Trp Lys Asp Ser Asp Val Leu Phe Cys His Ile His Pro Val Ser Val  
 225 230 235 240

Val Leu Ser Ser Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe  
 245 250 255

Val Gly Ser Phe Arg Lys Gln Trp Arg Xaa Gln His Pro Ile Leu Lys  
 260 265 270

Leu Ala Leu Gln Arg Ala Leu Gln Asp Ile Ala Glu Val Asp His Ser  
 275 280 285

Glu Gly Cys Phe Arg Gln Gly Thr Arg Arg Phe Lys Glu Ala Phe Trp  
 290 295 300

Cys Arg Asp Gly Pro Leu Tyr Phe His His Ile Tyr Val Ala Leu Arg  
 305 310 315 320

Gly Asn Phe Ala

<210> 59  
 <211> 578  
 <212> DNA  
 <213> H.Sapiens

<400> 59  
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 tggatctgat tctcaatggaa acaactgatt gaaagcaggc tgagattcga tcctgaatga 180  
 ccctcaagat atggaagggtt aaaaaacata cgtaaaatgc aaggagtagc agaatggta 240  
 gccttcgtgc tttctgctta aggcagctgt cagttgcag tccatgggtc aaagtgtgga 300  
 taatcgtggt atagcaaagt gtcactatca ccaaggggag gcagaaagta cttgcagtca 360  
 aaatcaggtt gtaccactta atagtattga gttcatccga actggtgagg tcgagacagg 420  
 ctgatctggtt ggtcctgttg gttgatgtga tcaagaaggt catcgaaatg acagctacca 480  
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 agcagctcat tgggtgaatg atcacacagt agcggaaag 578

<210> 60  
 <211> 192  
 <212> PRT  
 <213> H.Sapiens

<400> 60

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Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile His  
 1 5 10 15

Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile Ser  
 20 25 30

Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn Arg  
 35 40 45

Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu Asn  
 50 55 60

Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Ser Thr Phe Cys Leu  
 65 70 75 80

Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr Leu  
 85 90 95

Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg Arg  
 100 105 110

Leu Thr Ile Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro Phe  
 115 120 125

His Ile Leu Arg Val Ile Gln Asp Arg Ile Ser Ala Cys Phe Gln Ser  
 130 135 140

Val Val Pro Leu Arg Ile Arg Ser Met Lys Leu Thr Ser Phe Leu Asp  
 145 150 155 160

His Tyr Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Tyr Val Val  
 165 170 175

Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys Lys  
 180 185 190

<210> 61

<211> 872

<212> DNA

<213> H.Sapiens

<400> 61

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cctgcacaag	gctccttact	acttcctgct	ggacctgtgc	ctggccgatg	gcatacgctc	660
tgccgtctgc	ttcccccttg	tgctggcttc	tgtgcgccac	ggctcttcat	ggaccttcag	720
tgcactcagc	tgcaagattg	tggccttat	ggccgtgctc	ttttgcttcc	atgcggcctt	780
catgctgttc	tgcacagcgc	tcacccgcta	catggccatc	gccaccacc	gcttctacgc	840
caagcgcatg	acactctgga	catgcgcggc	tg			872

<210> 62  
 <211> 143  
 <212> PRT  
 <213> H.Sapiens

<400> 62

Met	Ala	Asn	Thr	Thr	Gly	Glu	Pro	Glu	Glu	Val	Ser	Gly	Ala	Leu	Ser
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Met	Cys	Val	Ser	Leu	Ala	Gly	Asn	Ala	Ile	Leu	Ser	Leu	Leu	Val	Leu
Lys	Glu	Arg	Ala	Leu	His	Lys	Ala	Pro	Tyr	Tyr	Phe	Leu	Leu	Asp	Leu
Cys	Leu	Ala	Asp	Gly	Ile	Arg	Ser	Ala	Val	Cys	Phe	Pro	Phe	Val	Leu
Ala	Ser	Val	Arg	His	Gly	Ser	Ser	Trp	Thr	Phe	Ser	Ala	Leu	Ser	Cys
Lys	Ile	Val	Ala	Phe	Met	Ala	Val	Leu	Phe	Cys	Phe	His	Ala	Ala	Phe
Met	Leu	Phe	Cys	Ile	Ser	Val	Thr	Arg	Tyr	Met	Ala	Ile	Ala	His	His
Arg	Phe	Tyr	Ala	Lys	Arg	Met	Thr	Leu	Trp	Thr	Cys	Ala	Ala	Glu	
130															

<210> 63  
 <211> 962  
 <212> DNA  
 <213> H.Sapiens

<400> 63

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tgatTTTactc	tttttattttt	cctcctaggt	ttctggata	agtatgtgca	aataaaaaat	180

aaacatgaga aggaactgta acctgattat ggatttggga aaaagataaa tcaacacaca 240  
 aaggaaaag taaactgatt gacagccctc aggaatgatg ccctttgcc acaatataat 300  
 taatatttcc tgtgtgaaaa acaactggtc aaatgatgtc cgtgcttccc tgtacagttt 360  
 aatggtgctc ataattctga ccacactcgt tggcaatctg atagttattt tttctatatc 420  
 acacttcaaa caacttcata ccccaacaaa ttggctcatt cattccatgg ccactgtgga 480  
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 tgtccctgct gttttgcat ttggaaatgat ctttctggag ctaaacttca aaggcgctga 780  
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 atctggggta ctgaccctta tgacttctt ttatataacct ggatcttattatgtgtgt 900  
 ctattacaga atatatctta tcgctaaaga acaggcaaga ttaatttagtg atgcaatca 960  
 ga 962

<210> 64  
 <211> 238  
 <212> PRT  
 <213> H.Sapiens

<400> 64

Arg Glu Lys Thr Asp Gln Pro Ser Gly Met Met Pro Phe Cys His Asn  
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Ile Ile Asn Ile Ser Cys Val Lys Asn Asn Trp Ser Asn Asp Val Arg  
20 25 30

Ala Ser Leu Tyr Ser Leu Met Val Leu Ile Ile Leu Thr Thr Leu Val  
35 40 45

Gly Asn Leu Ile Val Ile Val Ser Ile Ser His Phe Lys Gln Leu His  
50 55 60

Thr Pro Thr Asn Trp Leu Ile His Ser Met Ala Thr Val Asp Phe Leu  
65 70 75 80

Leu Gly Cys Leu Val Met Pro Tyr Ser Met Val Arg Ser Ala Glu His  
85 90 95

Cys Trp Tyr Phe Gly Glu Val Phe Cys Lys Ile His Thr Ser Thr Asp  
100 105 110

Ile Met Leu Ser Ser Ala Ser Ile Phe His Leu Ser Phe Ile Ser Ile

115

120

125

Asp Arg Tyr Tyr Ala Val Cys Asp Pro Leu Arg Tyr Lys Ala Lys Met  
 130 135 140

Asn Ile Leu Val Ile Cys Val Met Ile Phe Ile Ser Trp Ser Val Pro  
 145 150 155 160

Ala Val Phe Ala Phe Gly Met Ile Phe Leu Glu Leu Asn Phe Lys Gly  
 165 170 175

Ala Glu Glu Ile Tyr Tyr Lys His Val His Cys Arg Gly Gly Cys Ser  
 180 185 190

Val Phe Phe Ser Lys Ile Ser Gly Val Leu Thr Phe Met Thr Ser Phe  
 195 200 205

Tyr Ile Pro Gly Ser Ile Met Leu Cys Val Tyr Tyr Arg Ile Tyr Leu  
 210 215 220

Ile Ala Lys Glu Gln Ala Arg Leu Ile Ser Asp Ala Asn Gln  
 225 230 235

<210> 65  
 <211> 1018  
 <212> DNA  
 <213> H.Sapiens

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ctgCTTTta	ttattCCTGg	ttggATTGca	ccactACTca	gtttCTTATTt	tataATACTg	180
attataAAAC	atgggAGGGA	aataACTTTg	tattggTTTt	tatggATAAT	ttattATGTg	240
tcctAGACTc	tggCCTTgTC	aaaAGAAGGA	cgtaAGAAGG	cacgATgtat	tataCTTGGG	300
aatgATAGAA	gagACTgACC	tggTATTTC	accCGGAAGA	gggAAAGGAT	tttaACTACA	360
aatacAGGAA	tccAGCAGAT	ggcatCAGAG	aacACTATAA	aaaAGAAACG	atttGCAACA	420
gccACCTCTC	ttccAAAACA	attCCTTACT	tctgtGGTCT	gcaAGGCGGT	ttttGAATG	480
gaacAGAAACA	tagTAATATA	ggAAAACACA	atgATGAGAA	aAGCCAGCAA	gttCACACCT	540
gttggggAAA	agcacACTTT	taACATCTCA	ggcgtAAAAG	tcaACAGTAA	aATTACTGTG	600
gtacAGGTTG	agtATCCCTT	ACCCAAAATG	tttGAAACCA	gaaATGTTTt	ggattTCGGA	660
tttCGGAATA	tttACACATT	cataATGATA	tATCTTGGAA	atggTTCCCA	agtCTAAACA	720
caAAATTTAT	ttatGTTCA	tataCACCTT	atACACATAG	tctgAAAGTA	atTTTGTACA	780
atATTTAAA	taATTTGGG	CATGAAACAA	AGTTTGCATA	CATTGAACCA	TCAGACAGCA	840
aaAGCTTCAG	gtgtGGAATT	ttccACTTGT	ggcatCATGT	tGATGCTCAA	aaAGTTCCAT	900

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attttagagc atttcaaatt ttggattttc aaattacaaa tgcttaacct gtacttagat 960  
gttaaataca gtgcctcttc cacgggcact ttcaggaagc attctttat ataagccc 1018

<210> 66  
<211> 327  
<212> PRT  
<213> H.Sapiens

<400> 66

Tyr Ile Lys Glu Cys Phe Leu Lys Val Pro Val Glu Glu Ala Leu Tyr  
1 5 10 15

Leu Thr Ser Lys Tyr Arg Leu Ser Ile Cys Asn Leu Lys Ile Gln Asn  
20 25 30

Leu Lys Cys Ser Lys Ile Trp Asn Phe Leu Ser Ile Asn Met Met Pro  
35 40 45

Gln Val Glu Asn Ser Thr Pro Glu Ala Phe Ala Val Trp Phe Asn Val  
50 55 60

Cys Lys Leu Cys Phe Met Pro Lys Ile Ile Asn Ile Val Gln Asn Tyr  
65 70 75 80

Phe Gln Thr Met Cys Ile Arg Cys Ile Asn Ile Asn Lys Phe Cys Val  
85 90 95

Thr Trp Glu Pro Phe Pro Arg Tyr Ile Ile Met Asn Val Ile Phe Arg  
100 105 110

Asn Pro Lys Ser Lys Thr Phe Leu Val Ser Asn Ile Leu Gly Lys Gly  
115 120 125

Tyr Ser Thr Cys Thr Thr Val Ile Leu Leu Leu Thr Phe Thr Pro Glu  
130 135 140

Met Leu Lys Val Cys Phe Ser Pro Thr Gly Val Asn Leu Leu Ala Phe  
145 150 155 160

Leu Ile Ile Val Phe Ser Tyr Ile Thr Met Phe Cys Ser Ile Gln Lys  
165 170 175

Thr Ala Leu Gln Thr Thr Glu Val Arg Asn Cys Phe Gly Arg Glu Val  
180 185 190

Ala Val Ala Asn Arg Phe Phe Phe Ile Val Phe Ser Asp Ala Ile Cys  
195 200 205

Trp Ile Pro Val Phe Val Val Lys Ile Leu Ser Leu Phe Arg Val Glu  
210 215 220

Ile Pro Gly Gln Ser Leu Leu Ser Phe Pro Ser Ile Ile His Arg Ala  
225 230 235 240

Phe Leu Arg Pro Ser Phe Asp Lys Ala Arg Val Asp Thr Ile Ile His  
245 250 255

Lys Asn Gln Tyr Lys Val Ile Ser Leu Pro Cys Phe Ile Ile Ser Ile  
 260 265 270

Ile Lys Lys Leu Ser Ser Gly Ala Ile Gln Pro Gly Ile Ile Lys Ser  
 275 280 285

Arg Ser Tyr Arg Glu Thr Lys Ser Glu Tyr Leu Ala Ser Ile Ala Arg  
 290 295 300

His Trp Phe Phe Thr Arg Ser Met His Lys Thr Ile Lys Ile Tyr Met  
 305 310 315 320

Pro Arg Phe His Pro Gly Leu  
 325

<210> 67

<211> 1251

<212> DNA

<213> H.Sapiens

<400> 67

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gggctgccag ccaatgggtt	gatggcgtgg	ctggccggct	cccaggcccc	gcatggagct	180
ggcacgcgtc tggcgctgct	cctgctcagc	ctggccctct	ctgacttctt	gttcctggca	240
gcagcggcct tccagatcct	agagatccgg	catggggac	actggccgct	ggggacagct	300
gcctgccgct tctactactt	cctatggggc	gtgtcctact	cctccggcct	tttcctgctg	360
gccgcctca gcctcgaccg	ctgcctgctg	gcgctgtgcc	cacactggta	ccctggcac	420
cgcaggatcc gcctgcccct	ctgggtctgc	gccgggtct	gggtgctggc	cacactttc	480
agcgtgccct ggctggtctt	ccccgaggct	gccgtctgg	ggtacgacct	ggtcatctgc	540
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tgccaccggcc aacagcagcc	cgcagcctgc	cggggcttcg	cccgtgtggc	caggaccatt	720
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ggcagcttca cgcccactga	gccacagacc	cagctagatt	ctgagggtcc	aactctgcca	1020
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acactccagc cacgatcgga	tcccacagct	cagccacagc	tgaaccctac	ggcccagcca	1140

cagtcggatc ccacagccca gccacagctg aacctcatgg cccagccaca gtcagattct 1200  
 gtggcccagc cacaggcaga cactaacgtc cagacccttg cacctgctgc c 1251

<210> 68  
 <211> 417  
 <212> PRT  
 <213> H.Sapiens

<400> 68

Thr Thr Met Glu Ala Asp Leu Gly Ala Thr Gly His Arg Pro Arg Thr  
 1 5 10 15

Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly Gly Trp Asp Thr Val  
 20 25 30

Phe Leu Val Ala Leu Leu Leu Leu Gly Leu Pro Ala Asn Gly Leu Met  
 35 40 45

Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly Ala Gly Thr Arg Leu  
 50 55 60

Ala Leu Leu Leu Leu Ser Leu Ala Leu Ser Asp Phe Leu Phe Leu Ala  
 65 70 75 80

Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His Gly Gly His Trp Pro  
 85 90 95

Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe Leu Trp Gly Val Ser  
 100 105 110

Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu Ser Leu Asp Arg Cys  
 115 120 125

Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly His Arg Pro Val Arg  
 130 135 140

Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val Leu Ala Thr Leu Phe  
 145 150 155 160

Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala Val Trp Trp Tyr Asp  
 165 170 175

Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu Glu Leu Ser Leu Arg  
 180 185 190

Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe Leu Leu Leu Val  
 195 200 205

Cys His Val Leu Thr Gln Ala Thr Ala Cys Arg Thr Cys His Arg Gln  
 210 215 220

Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg Val Ala Arg Thr Ile  
 225 230 235 240

Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr Gln Leu Ala Gln Leu

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245

250

255

Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu Leu Trp  
260 265 270

Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser Cys Leu  
275 280 285

Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr Leu Leu  
290 295 300

Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu Arg Pro  
305 310 315 320

Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser Glu Gly  
325 330 335

Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met Asp Pro  
340 345 350

Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser Asp Pro  
355 360 365

Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser Asp Pro  
370 375 380

Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser Asp Ser  
385 390 395 400

Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln Thr Pro Ala Pro Ala  
405 410 415

Ala

<210> 69  
<211> 659  
<212> DNA  
<213> H.Sapiens

<400> 69  
tacaggcctg agcatgctgg gctccatca gaccaaggac tgcctgtcca tcctgtggcc 60  
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ccctgtccct gctgcagagc atcctgaaat ggatgttctg tggcttcctg tctagtggtg 180  
ctgattctgt ttggtgtgaa acatcagatt tcatcacagt cacatggctg attttttat 240  
gtgtggttct ctgcgggtcc agcccggttc tgctggtcag gatcctttgt ggatcccgga 300  
agatgccctt gaccaggctg tacatgacca tcctgctcag agtgctggtc ttcctccct 360  
gtgacctgcc ctttggcatt cagtgattcc tattttctg gatccacgtg gatttgtcac 420  
gttcgtctag tttccatttt cctgtccact cttaacagca gtgccaaccc cattattac 480  
ttcttcatgg gtcctttag gcagcttcaa aacaggaaga ctctctagct gttctccag 540

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agggctctgc aggacacgccc tgaggtggaa gaaggcagat ggcggctttc tgagggaaacc 600  
ctggagctgt catgaagcag attggggcca tgaggaagag cctctgcctt gtcagtcag 659

<210> 70  
<211> 213  
<212> PRT  
<213> H.Sapiens

<400> 70

Tyr Arg Pro Glu His Ala Gly Leu His Gln His Gln Ala Leu Pro Val  
1 5 10 15

His Pro Val Ala His Leu Val Pro Leu Pro Pro Pro His Thr Pro Val  
20 25 30

Ser Ser Arg Val Ser Cys Ser Gly Pro Cys Pro Cys Cys Arg Ala Ser  
35 40 45

Trp Asn Gly Cys Ser Val Ala Ser Cys Leu Val Val Leu Ile Leu Phe  
50 55 60

Gly Val Lys His Gln Ile Ser Ser Gln Ser His Gly Phe Phe Tyr Val  
65 70 75 80

Trp Phe Ser Ala Gly Pro Ala Arg Phe Cys Trp Ser Gly Ser Phe Val  
85 90 95

Asp Pro Gly Arg Cys Pro Pro Gly Cys Thr Pro Ser Cys Ser Glu Cys  
100 105 110

Trp Ser Ser Ser Val Thr Cys Pro Leu Ala Phe Ser Asp Ser Tyr  
115 120 125

Phe Ser Gly Ser Thr Trp Ile Cys His Val Arg Leu Val Ser Ile Phe  
130 135 140

Leu Ser Thr Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe Met  
145 150 155 160

Gly Ser Phe Arg Gln Leu Gln Asn Arg Lys Thr Leu Leu Val Leu Gln  
165 170 175

Arg Ala Leu Gln Asp Thr Pro Glu Val Glu Glu Gly Arg Trp Arg Leu  
180 185 190

Ser Glu Glu Thr Leu Glu Leu Ser Ser Arg Leu Gly Pro Gly Arg Ala  
195 200 205

Ser Ala Leu Ser Val  
210

<210> 71  
<211> 559  
<212> DNA  
<213> H.Sapiens

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<400> 71 atgccgaagg caggccgcag aagagaagag gaggacggtg aggaggatga gcccaggaa 60  
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cccacacatg gtgcaacaca gcagagccag cagcaccgct gccaccagcc acagcgtccg 180  
gcacaagtgg cggctgggct cccccaaagaa ctgggtgcag gcgcccgtga gcagcaggtg 240  
cagcagcagg cagagggccc aggtgagggc gcacacacag gtggtcaggt ggcgtggcg 300  
gcggcacgag taccaggctg ggaagagggc ggccaggcac tgctccacgc tgacggccgc 360  
caggagactc aggcccacga tgttagcagaa gaagcgcagc gttgccaggc tggctctgcac 420  
gaagccccggg aagtccagcc ggccttgcag caagtcgggg acgatggcca ccatgtggca 480  
gccaaggaaag atgagatccg cgcaggccac gtccaggagg tagatggcga aagggtttct 540  
qtaqacattq qaqctqaqc 559

<210> 72  
<211> 211  
<212> PRT  
<213> H.Sapiens

<400> 72

Leu Ser Ser Asn Val Tyr Arg Asn Pro Phe Ala Ile Tyr Leu Leu Asp  
1 5 10 15

Val Ala Cys Ala Asp Leu Ile Phe Leu Gly Cys His Met Val Ala Ile  
20 25 30

Val Pro Asp Leu Leu Gln Gly Arg Leu Asp Phe Pro Gly Phe Val Gln  
35 40 45

Thr Ser Leu Ala Thr Leu Arg Phe Phe Cys Tyr Ile Val Gly Leu Ser  
50 55 60

Leu Leu Ala Ala Val Ser Val Glu Gln Cys Leu Ala Ala Leu Phe Pro  
65 70 75 80

Ala Trp Tyr Ser Cys Arg Arg Pro Arg His Leu Thr Thr Cys Val Cys  
85 90 95

Ala Leu Thr Trp Ala Leu Cys Leu Leu Leu His Leu Thr Thr Cys Val  
 100 105 110

Cys Ala Leu Thr Trp Ala Leu Cys Leu Leu Leu His Leu Leu Leu Ser  
115 120 125

Gly Ala Cys Thr Leu Leu Leu Ser Gly Ala Cys Thr Gln Phe Phe Gly  
130 135 140

Glu Pro Ser Arg His Leu Cys Arg Thr Leu Trp Leu Val Ala Ala Val  
145 150 155 160

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Leu Leu Ala Leu Leu Cys Cys Thr Met Cys Gly Ala Ser Leu Met Leu  
 165 170 175

Leu Leu Arg Val Glu Arg Gly Pro Gln Arg Pro Pro Pro Arg Gly Phe  
 180 185 190

Pro Gly Leu Ile Leu Leu Thr Val Leu Leu Phe Ser Ser Ala Ala Cys  
 195 200 205

Leu Arg His  
 210

<210> 73  
 <211> 1008  
 <212> DNA  
 <213> H.Sapiens

<400> 73  
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 ctctgcttca ctttgcattct ggctgtggct gacacccattga ttgggtgtggc catctctggc 120  
 ctactcacag accagctctc cagcccttct cggcccacac agaagaccct gtgcagcctg 180  
 cggatggcat ttgtcacttc ctccgcagct gcctctgtcc tcacggtcat gctgatcacc 240  
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 gaacggtacc tgtggctgct cggcgtgggc aactccctgc tcaacccact catctatgcc 780  
 tattggcaga aggaggtgcg actgcagctc taccacatgg ccctaggagt gaagaagg 840  
 ctcacccat tcctccttct tctctggcc aggaattgtg gcccagagag gcccaggaa 900  
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 atggctaa

<210> 74  
 <211> 335  
 <212> PRT  
 <213> H.Sapiens

<400> 74

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Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala Ser  
 1 5 10 15

Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu  
 20 25 30

Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala  
 35 40 45

Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp  
 50 55 60

Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu  
 65 70 75 80

Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val  
 85 90 95

Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg  
 100 105 110

Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly  
 115 120 125

Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro  
 130 135 140

Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val  
 145 150 155 160

Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro  
 165 170 175

Ala Met Leu Leu Phe Val Phe Tyr Cys Asp Met Leu Lys Ile Ala  
 180 185 190

Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met  
 195 200 205

Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu  
 210 215 220

Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro  
 225 230 235 240

Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu  
 245 250 255

Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser  
 260 265 270

Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu  
 275 280 285

Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe  
 290 295 300

Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu

305

310

315

320

Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly  
325 330 335

<210> 75  
<211> 2137  
<212> DNA  
<213> *H. Sapiens*

<400> 75 aactggaaagg gcagccgtct gccgcccacg aacaccttct caagcacttt gagtgaccac 60 ggcttgcaga ctgggtggctg gccccccgag tcccgggctc tgagggcacgg ccgtcgactt 120 aagcgttgca tcctgttacc tggagaccct ctgagctctc acctgctact tctgccgctg 180 cttctgcaca gagcccgggc gaggaccct ccagggatgca ggtcccgaac agcaccggcc 240 cgagacaacgc gacgctgcag atgctgcgga accccggcgat cgccggtgcc ctgcccgtgg 300 tgtactcgct ggtggcgccg gtcagcatcc cgggcaacct cttctctctg tgggtgctgt 360 gccggcgcat gggggccaga tccccgtcgg tcatcttcat gatcaacctg agcgtcacgg 420 acctgatgct gcccagcgtg ttgcctttcc aaatctacta ccattgcaac cgccaccact 480 gggtattcgg ggtgctgctt tgcaacgtgg tgaccgtggc ctttacgca aacatgtatt 540 ccagcatcct caccatgacc tgtatcagcg tggagcgcctt cctgggggtc ctgtaccgc 600 tcagctccaa gcgctggcgc cgccgtcggt acgcgggtggc cgctgtgca gggacctggc 660 tgctgtccct gaccggccctg tccccgtcgg cgccgaccga tctcacctac ccgggtgcacg 720 ccctggcat catcacctgc ttgcacgtcc tcaagtggac gatgctcccc agcgtggcca 780 tgtggggcgt gttccttttc accatcttca tcctgtcttt cctcatcccg ttcgtgtatca 840 ccgtggctt gtagacggcc accatcctca agctgttgcg cacggaggag ggcacggcc 900 gggagcagcg gagggcgccg gtggggctgg ccgcgggtgg cttgctggcc tttgtcacct 960 gcttcggcccc caacaacttc gtgctccctgg cgacatcgat gagccgcctg ttctacggca 1020 agagctacta ccacgtgtac aagctcacgc tgtgtctcag ctgcctcaac aactgtctgg 1080 acccgtttgtt ttattacttt gcgtccccggg aattccagct ggcgcgtgg gaatatttgg 1140 gctggccccc ggtgcccaga gacaccctgg acacgcgcgg cgagagcctc ttctccggca 1200 ggaccacgtc cgtgcgttcc gaggccggtg cgccaccctga agggatggag ggagccacca 1260 ggcccgccct ccagaggcag gagagtgtgt tctgagtcctt gggggcgccag cttggagagc 1320 cggggcgca gcttggagga tccagggcg catggagagg ccacgggtgcc agaggttcag 1380 ggagaacagc tgcgttgctc ccaggcaactg cagaggcccg gtggggaaagg gtctccaggc 1440

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tttttagtag	agctgggctg	tcaccccgaa	gctccttaga	cactcctcac	acctgtccat	1680
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gcccggtgca	cggcgaaatt	tctgtttatt	tcactcaggg	gcactgtggt	tgctgtggtt	2040
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<210> 76  
<211> 359  
<212> PRT  
<213> H.Sapiens

<400> 76

Met	Gln	Val	Pro	Asn	Ser	Thr	Gly	Pro	Asp	Asn	Ala	Thr	Leu	Gln	Met
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					20				25				30		
Val	Ala	Ala	Val	Ser	Ile	Pro	Gly	Asn	Leu	Phe	Ser	Leu	Trp	Val	Leu
					35			40				45			
Cys	Arg	Arg	Met	Gly	Pro	Arg	Ser	Pro	Ser	Val	Ile	Phe	Met	Ile	Asn
			50			55				60					
Leu	Ser	Val	Thr	Asp	Leu	Met	Leu	Ala	Ser	Val	Leu	Pro	Phe	Gln	Ile
						65			70			75			80
Tyr	Tyr	His	Cys	Asn	Arg	His	His	Trp	Val	Phe	Gly	Val	Leu	Leu	Cys
								85		90			95		
Asn	Val	Val	Thr	Val	Ala	Phe	Tyr	Ala	Asn	Met	Tyr	Ser	Ser	Ile	Leu
									100	105				110	
Thr	Met	Thr	Cys	Ile	Ser	Val	Glu	Arg	Phe	Leu	Gly	Val	Leu	Tyr	Pro
								115	120				125		
Leu	Ser	Ser	Lys	Arg	Trp	Arg	Arg	Arg	Tyr	Ala	Val	Ala	Ala	Cys	
									130	135			140		

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Ala Gly Thr Trp Leu Leu Leu Thr Ala Leu Ser Pro Leu Ala Arg  
145 150 155 160

Thr Asp Leu Thr Tyr Pro Val His Ala Leu Gly Ile Ile Thr Cys Phe  
165 170 175

Asp Val Leu Lys Trp Thr Met Leu Pro Ser Val Ala Met Trp Ala Val  
180 185 190

Phe Leu Phe Thr Ile Phe Ile Leu Leu Phe Leu Ile Pro Phe Val Ile  
195 200 205

Thr Val Ala Cys Tyr Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu  
210 215 220

Glu Ala His Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala  
225 230 235 240

Val Val Leu Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val  
245 250 255

Leu Leu Ala His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr  
260 265 270

His Val Tyr Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu  
275 280 285

Asp Pro Phe Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu  
290 295 300

Arg Glu Tyr Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr  
305 310 315 320

Arg Arg Glu Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu  
325 330 335

Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu  
340 345 350

Gln Arg Gln Glu Ser Val Phe  
355

<210> 77  
<211> 1197  
<212> DNA  
<213> H.Sapiens

<400> 77  
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gtgggtgtgcc tggcggtgtg cgccttcatc gtgctagaga atctagccgt gttgtggtg 180  
ctcggacgccc acccgcgctt ccacgctccc atgttccctgc tcctggcag cctcacgttg 240  
tcggatctgc tggcaggcgc cgcctacgccc gccaacatcc tactgtcgaa gccgctcactc 300  
ctgaaactgt ccccccgcgt ctggttcgca cgggagggag gctgtttcggt ggcactcact 360

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gcgtccgtgc	tgagcctcct	ggccatcgcg	ctggagcgca	gcctcaccat	ggcgccgagg	420
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acctgtcctg	tactcctgca	ggccgatccc	ttcctggac	tggccatggc	caactcactt	900
ctgaacccca	tcatctacac	gctcaccaac	cgcgacctgc	gccacgcgc	cctgcgcctg	960
gtctgctgcg	gacgccactc	ctgcggcaga	gacccgagtg	gctcccagca	gtcggcgagc	1020
gcggctgagg	cttccgggg	cctgcgcccgc	tgcctgcccc	cgggccttga	tggagcttc	1080
agcggctcg	agcgctcatc	gccccagcgc	gacgggctgg	acaccagcgg	ctccacagggc	1140
agccccggtg	cacccacacgc	cgcccgact	ctggtatcag	aaccggctgc	agactga	1197

<210> 78  
 <211> 398  
 <212> PRT  
 <213> H.Sapiens

<400> 78

Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val  
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Leu His Tyr Asn Tyr, Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro  
 20 25 30

Gly Ala Gly Leu Arg Ala Asp Ala Val Val Cys Leu Ala Val Cys Ala  
 35 40 45

Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His  
 50 55 60

Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu  
 65 70 75 80

Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Ala Asn Ile Leu Leu Ser  
 85 90 95

Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu  
 100 105 110

Gly Gly Val Phe Val Ala Leu Thr Ala Ser Val Leu Ser Leu Leu Ala

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115

120

125

Ile Ala Leu Glu Arg Ser Leu Thr Met Ala Arg Arg Gly Pro Ala Pro  
130 135 140

Val Ser Ser Arg Gly Arg Thr Leu Ala Met Ala Ala Ala Ala Trp Gly  
145 150 155 160

Val Ser Leu Leu Leu Gly Leu Leu Pro Ala Leu Gly Trp Asn Cys Leu  
165 170 175

Gly Arg Leu Asp Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys Ala  
180 185 190

Tyr Val Leu Phe Cys Val Leu Ala Phe Val Gly Ile Leu Ala Ala Ile  
195 200 205

Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln Val Arg Ala Asn Ala Arg  
210 215 220

Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly Thr Thr Ser Thr Arg Ala  
225 230 235 240

Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val Val  
245 250 255

Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu  
260 265 270

Leu Asp Val Ala Cys Pro Ala Arg Thr Cys Pro Val Leu Leu Gln Ala  
275 280 285

Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro Ile  
290 295 300

Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg Leu  
305 310 315 320

Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser Gly Ser Gln  
325 330 335

Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg Arg Cys Leu  
340 345 350

Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg Ser Ser Pro  
355 360 365

Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser Pro Gly Ala  
370 375 380

Pro Thr Ala Ala Arg Thr Leu Val Ser Glu Pro Ala Ala Asp  
385 390 395

<210> 79

<211> 1041

<212> DNA

<213> H.Sapiens

<400> 79

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gatttcctcc	ttatgatctg	cctgcctttt	cggacagact	attacctcag	acgttagacac	240
tgggctttg	gggacattcc	ctgcccagtg	gggctttca	cgttggccat	gaacagggcc	300
gggagcatcg	tgttccttac	ggtggggct	gcggacaggt	atttcaaagt	ggtccacccc	360
caccacgcgg	tgaacactat	ctccacccgg	gtggcggtc	gcatcgctg	caccctgtgg	420
gccctggta	tcctggaaac	agtgtatctt	ttgctggaga	accatctctg	cgtgcaagag	480
acggccgtct	cctgtgagag	cttcatcatg	gagtcggcca	atggctggca	tgacatcatg	540
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cacataaccc	ttagcttcac	ctacatgaac	agcatgtgg	atcccctgg	gtattattt	840
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cagccaggac	actcaaaaac	acaaaggccg	gaagagatgc	caatttcgaa	cctcggcgc	960
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<210> 80  
 <211> 346  
 <212> PRT  
 <213> H.Sapiens

<400> 80

Met	Tyr	Asn	Gly	Ser	Cys	Cys	Arg	Ile	Glu	Gly	Asp	Thr	Ile	Ser	Gln
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Val	Met	Pro	Pro	Leu	Leu	Ile	Val	Ala	Phe	Val	Leu	Gly	Ala	Leu	Gly
							20			25			30		

Asn	Gly	Val	Ala	Leu	Cys	Gly	Phe	Cys	Phe	His	Met	Lys	Thr	Trp	Lys
								35		40		45			

Pro	Ser	Thr	Val	Tyr	Leu	Phe	Asn	Leu	Ala	Val	Ala	Asp	Phe	Leu	Leu
							50		55		60				

Met	Ile	Cys	Leu	Pro	Phe	Arg	Thr	Asp	Tyr	Tyr	Leu	Arg	Arg	Arg	His
65								70		75					80

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Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala  
85 90 95

Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp  
100 105 110

Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser  
115 120 125

Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile  
130 135 140

Leu Gly Thr Val Tyr Leu Leu Glu Asn His Leu Cys Val Gln Glu  
145 150 155 160

Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp  
165 170 175

His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile  
180 185 190

Leu Phe-Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln  
195 200 205

Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val  
210 215 220

Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg  
225 230 235 240

Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val  
245 250 255

His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met  
260 265 270

Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe  
275 280 285

Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His  
290 295 300

Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg  
305 310 315 320

Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly  
325 330 335

Gln Trp Asp Pro His Ile Val Glu Trp His  
340 345

<210> 81

<211> 2525

<212> DNA

<213> H.Sapiens

<400> 81

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ccatggcggt	cattaacttg	gtgggtggtcc	acagcgttt	tctgctgaca	gtgccatttc	240
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gtgccatgt	gcacatccac	atgtacctca	cgttcctatt	ctatgtggtg	atcctggtca	360
ccagataacct	catcttcttc	aagtgc当地	acaaagtgg	attctacaga	aaactgc当地	420
ctgtggctgc	cagtgc当地	atgtggacgc	tggtgattgt	cattgtggta	cccctggttg	480
tctcccggt	tggaatccat	gaggaataca	atgaggagca	ctgtttaaa	tttcacaaaag	540
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ttccggcggtt	aaaattatat	atatatata	ttaaattata	ccttaagttc	tggggtacat	1920
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gtcaacccat	ctacattagg	tatttctcct	aatgctctcc	ctccccctagc	ccccccacccc	2040
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tcttt						2525

<210> 82  
 <211> 312  
 <212> PRT  
 <213> H.Sapiens

<400> 82

Met Thr Gly Asp Phe Pro Ser Met Pro Gly His Asn Thr Ser Arg Asn  
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Ser Ser Cys Asp Pro Ile Val Thr Pro His Leu Ile Ser Leu Tyr Phe  
 20 25 30

Ile Val Leu Ile Gly Gly Leu Val Gly Val Ile Ser Ile Leu Phe Leu  
 35 40 45

Leu Val Lys Met Asn Thr Arg Ser Val Thr Thr Met Ala Val Ile Asn  
 50 55 60

Leu Val Val Val His Ser Val Phe Leu Leu Thr Val Pro Phe Arg Leu  
 65 70 75 80

Thr Tyr Leu Ile Lys Lys Thr Trp Met Phe Gly Leu Pro Phe Cys Lys  
 85 90 95

Phe Val Ser Ala Met Leu His Ile His Met Tyr Leu Thr Phe Leu Phe  
 100 105 110

Tyr Val Val Ile Leu Val Thr Arg Tyr Leu Ile Phe Phe Lys Cys Lys  
 115 120 125

Asp Lys Val Glu Phe Tyr Arg Lys Leu His Ala Val Ala Ala Ser Ala  
 130 135 140

Gly Met Trp Thr Leu Val Ile Val Val Val Pro Leu Val Val Ser  
 145 150 155 160

Arg Tyr Gly Ile His Glu Glu Tyr Asn Glu Glu His Cys Phe Lys Phe  
 165 170 175

His Lys Glu Leu Ala Tyr Thr Tyr Val Lys Ile Ile Asn Tyr Met Ile  
 180 185 190

Val Ile Phe Val Ile Ala Val Ala Val Ile Leu Leu Val Phe Gln Val  
 195 200 205

Phe Ile Ile Met Leu Met Val Gln Lys Leu Arg His Ser Leu Leu Ser  
 210 215 220

His Gln Glu Phe Trp Ala Gln Leu Lys Asn Leu Phe Phe Ile Gly Val  
 225 230 235 240

Ile Leu Val Cys Phe Leu Pro Tyr Gln Phe Phe Arg Ile Tyr Tyr Leu  
 245 250 255

Asn Val Val Thr His Ser Asn Ala Cys Asn Ser Lys Val Ala Phe Tyr  
 260 265 270

Asn Glu Ile Phe Leu Ser Val Thr Ala Ile Ser Cys Tyr Asp Leu Leu  
 275 280 285

Leu Phe Val Phe Gly Gly Ser His Trp Phe Lys Gln Lys Ile Ile Gly  
 290 295 300

Leu Trp Asn Cys Val Leu Cys Arg  
 305 310

<210> 83

<211> 1125

<212> DNA

<213> H.Sapiens

<400> 83

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cagctgtgct acgcgaacgt gaatgggtcc tgtgtaaaa tcccctctc gcccggatcc 180

cgggtgattc tgtacatagt gtttggcttt ggggctgtgc tggctgtgtt tggaaacctc 240

ctgggtatga tttcaatcct ccatttcaag cagctgcact ctccgaccaa ttttctcggt 300

gcctctctgg cctgcgctga tttcttggtg ggtgtgactg tcatgcctt cagcatggc 360

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attatgataa ttctgtatgg taacatattt cttgtggcta gacgacaggc gaaaaagata	780
gaaaatactg gtagcaagac agaatcatcc tcagagagtt acaaagccag agtggccagg	840
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ttaccatata gcattgattc attaattgtat gctttatgg gcttataac ccctgcctgt	960
atttatgaga tttgctgttg gtgtgcttat tataactcag ccatgaatcc tttgatttat	1020
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aagaacagtt cagcaaccat gaatttgcgtt tctgaacata tataa	1125

<210> 84  
 <211> 345  
 <212> PRT  
 <213> H.Sapiens  
 <400> 84

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Val Ile Leu Tyr Ile Val Phe Gly Phe Gly Ala Val Leu Ala Val Phe	
35 40 45	
Gly Asn Leu Leu Val Met Ile Ser Ile Leu His Phe Lys Gln Leu His	
50 55 60	
Ser Pro Thr Asn Phe Leu Val Ala Ser Leu Ala Cys Ala Asp Phe Leu	
65 70 75 80	
Val Gly Val Thr Val Met Pro Phe Ser Met Val Arg Thr Val Glu Ser	
85 90 95	
Cys Trp Tyr Phe Gly Arg Ser Phe Cys Thr Phe His Thr Cys Cys Asp	
100 105 110	
Val Ala Phe Cys Tyr Ser Ser Leu Phe His Leu Cys Phe Ile Ser Ile	
115 120 125	
Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Val Tyr Pro Thr Lys Phe	
130 135 140	
Thr Val Ser Val Ser Gly Ile Cys Ile Ser Val Ser Trp Ile Leu Pro	
145 150 155 160	
Leu Met Tyr Ser Gly Ala Val Phe Tyr Thr Gly Val Tyr Asp Asp Gly	
165 170 175	

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Leu Glu Glu Leu Ser Asp Ala Leu Asn Cys Ile Gly Gly Cys Gln Thr  
 180 185 190

Val Val Asn Gln Asn Trp Val Leu Thr Asp Phe Leu Ser Phe Phe Ile  
 195 200 205

Pro Thr Phe Ile Met Ile Ile Leu Tyr Gly Asn Ile Phe Leu Val Ala  
 210 215 220

Arg Arg Gln Ala Lys Lys Ile Glu Asn Thr Gly Ser Lys Thr Glu Ser  
 225 230 235 240

Ser Ser Glu Ser Tyr Lys Ala Arg Val Ala Arg Arg Glu Arg Lys Ala  
 245 250 255

Ala Lys Thr Leu Gly Val Thr Val Val Ala Phe Met Ile Ser Trp Leu  
 260 265 270

Pro Tyr Ser Ile Asp Ser Leu Ile Asp Ala Phe Met Gly Phe Ile Thr  
 275 280 285

Pro Ala Cys Ile Tyr Glu Ile Cys Cys Trp Cys Ala Tyr Tyr Asn Ser  
 290 295 300

Ala Met Asn Pro Leu Ile Tyr Ala Leu Phe Tyr Pro Trp Phe Arg Lys  
 305 310 315 320

Ala Ile Lys Val Ile Val Thr Gly Gln Val Leu Lys Asn Ser Ser Ala  
 325 330 335

Thr Met Asn Leu Phe Ser Glu His Ile  
 340 345

<210> 85

<211> 1020

<212> DNA

<213> H.Sapiens

<400> 85

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tatggcatta tcttcctcgt gggatttcca ggcaatgcag tagtgatatac cacttacatt 180

ttcaaaatga gaccttggaa gagcagcacc atcattatgc tgaacctggc ctgcacagat 240

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atctttggag atttcatgtg taagtttac cgttcagct tccatttcaa cctgtatagc 360

agcatcctct tcctcacctg tttcagcatc ttccgctact gtgtgatcat tcacccaaatg 420

agctgctttt ccattcacaa aactcgatgt gcagttgtag cctgtgctgt ggtgtggatc 480

atttcactgg tagctgtcat tccgatgacc ttcttgatca catcaaccaa caggaccaac 540

agatcagcct gtctcgaccc caccagttcg gatgaactca atactattaa gtggtaaac 600

ctgattttga	ctgcaagttac	tttctgcctc	cccttggtga	tagtgacact	ttgctatacc	660
acgatttatcc	acactttgac	ccatggactg	caaactgaca	gctgccttaa	gcagaaagca	720
cgaaggctaa	ccattctgct	actccttgca	ttttacgtat	gttttttacc	cttccatatac	780
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<210> 86  
 <211> 336  
 <212> PRT  
 <213> H.Sapiens

<400> 86

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				20			25					30			
Met	His	Tyr	Leu	Pro	Val	Ile	Tyr	Gly	Ile	Ile	Phe	Leu	Val	Gly	Phe
				35			40				45				
Pro	Gly	Asn	Ala	Val	Val	Ile	Ser	Thr	Tyr	Ile	Phe	Lys	Met	Arg	Pro
				50			55				60				
Trp	Lys	Ser	Ser	Thr	Ile	Ile	Met	Leu	Asn	Leu	Ala	Cys	Thr	Asp	Leu
				65			70				75		80		
Leu	Tyr	Leu	Thr	Ser	Leu	Pro	Phe	Leu	Ile	His	Tyr	Tyr	Ala	Ser	Gly
				85				90				95			
Glu	Asn	Trp	Ile	Phe	Gly	Asp	Phe	Met	Cys	Lys	Phe	Ile	Arg	Phe	Ser
			100				105				110				
Phe	His	Phe	Asn	Leu	Tyr	Ser	Ser	Ile	Leu	Phe	Leu	Thr	Cys	Phe	Ser
				115			120				125				
Ile	Phe	Arg	Tyr	Cys	Val	Ile	Ile	His	Pro	Met	Ser	Cys	Phe	Ser	Ile
				130			135				140				
His	Lys	Thr	Arg	Cys	Ala	Val	Val	Ala	Cys	Ala	Val	Val	Trp	Ile	Ile
				145			150				155		160		
Ser	Leu	Val	Ala	Val	Ile	Pro	Met	Thr	Phe	Leu	Ile	Thr	Ser	Thr	Asn
					165			170			175				
Arg	Thr	Asn	Arg	Ser	Ala	Cys	Leu	Asp	Leu	Thr	Ser	Ser	Asp	Glu	Leu
				180				185			190				

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Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Ser Thr Phe Cys  
 195 200 205

Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr  
 210 215 220

Leu Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg  
 225 230 235 240

Arg Leu Thr Ile Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro  
 245 250 255

Phe His Ile Leu Arg Val Ile Gln Asp Arg Ile Ser Ala Cys Phe Gln  
 260 265 270

Ser Val Val Pro Leu Arg Ile Arg Ser Met Lys Leu Thr Ser Phe Leu  
 275 280 285

Asp His Tyr Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val  
 290 295 300

Val Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys  
 305 310 315 320

Lys Val Ser Gly Asn Leu Glu Gln Ala Lys Lys Ile Ser Tyr Ser Asn  
 325 330 335

<210> 87  
 <211> 1138  
 <212> DNA  
 <213> H.Sapiens

<400> 87  
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 tattcttcaa cagagagtaa tagttaaatg ttttagaagt gagaggactc aaattgccaa 120  
 tgatttactc ttttattttt ctccttagt ttctggata agtatgtgca aataaaaaat 180  
 aaacatgaga aggaactgta acctgattat ggatttggaa aaaagataaa tcaacacaca 240  
 aaggaaaaag taaactgatt gacagccctc aggaatgatg ccctttgcc acaatataat 300  
 taatatttcc tgtgtaaaaa acaactggtc aaatgatgtc cgtgcttccc tgtacagtt 360  
 aatggtgctc ataattctga ccacactcgt tggcaatctg atagttattt tttctatatc 420  
 acacttcaaa caacttcata ccccaacaaa ttggctcatt cattccatgg ccactgtgga 480  
 ctttcttctg ggggtctgg tcatgcctta cagtaggtg agatctgctg agcactgttg 540  
 gtattttggaa gaagtcttct gtaaaattca cacaagcacc gacattatgc tgagctcagc 600  
 ctccattttc catttgtctt tcatctccat tgaccgctac tatgctgtgt gtgatccact 660  
 gagatataaa gccaagatga atatcttgggt tatttgtgtg atgatcttca ttagttggag 720  
 tgtccctgct gtttttgcat ttggaaatgat ctttctggag ctaaaacttca aaggcgctga 780

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Val Tyr Tyr Arg Ile Tyr Leu Ile Ala Lys Glu Gln Ala Arg Leu Ile  
210 215 220

Ser Asp Ala Asn Gln Lys Leu Gln Ile Gly Leu Glu Met Lys Asn Gly  
225 230 235 240

Ile Ser Gln Ser Lys Glu Arg Lys Ala Val Lys Thr Leu Gly Ile Val  
245 250 255

Met Gly Val Phe Leu Ile Cys Trp Cys Pro Phe Phe Ile Cys Thr Val  
260 265 270

Met Asp Pro Phe Leu His Tyr Ile Ile Pro Pro Thr Leu Asn Asp Ala  
275 280 285

Arg Gly Ser Arg Ala Asn Ser Ala  
290 295

<210> 89

<211> 1023

<212> DNA

<213> H.Sapiens

<400> 89  
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aatgatgtcc gtgcttcct gtacagttt atgggtgtca taattctgac cacactcg 120  
ggcaatctga tagttattgt ttctatatca cacttcaaac aacttcatac cccaa 180  
tggctcattc attccatggc cactgtggac tttcttctgg ggtgtctggg catgcctt 240  
agtatggtga gatctgctga gcactgtgg tattttggag aagtcttctg taaaattc 300  
acaaggcaccc acattatgct gagctcagcc tccattttcc atttgccttt catctcc 360  
gaccgctact atgctgtgtg tcatccactg agatataaag ccaagatgaa tatcttgg 420  
atttgcgtga tgatcttcat tagttggagt gtcctgctg ttttgcatt tggaaatgatc 480  
tttctggagc taaacttcaa aggccgtgaa gagatataatt acaaacatgt tcactgc 540  
ggaggttgc ctgtcttctt tagcaaaata tctgggtac tgacctttat gacttctt 600  
tatatacctg gatctattat gttatgtgtc tattacagaa tatactttat cgctaaagaa 660  
caggcaagat taattagtga tgccaatcag aagctccaaa ttggattgga aatggaaaat 720  
ggaatttcac aaagcaaaga aaggaaagct gtgaagacat tggggattgt gatggagtt 780  
ttccataat gctggtgccc ttctttatc tgtacagtca tggacccttt tcttcactac 840  
attattccac ctacttgaa tcatgtattt atttggtttgc gctacttgaa ctctacattt 900  
aatccaatgg tttatgcatt ttctatcct tggtttagaa aagcactgaa gatgtatgt 960  
tttggtaaaa tttccaaaaa agattcatcc aggtgtaaat tattttggaa attgagttca 1020  
tag 1023

<210> 90  
<211> 339  
<212> PRT  
<213> H.Sapiens

<400> 90

Met Met Pro Phe Cys His Asn Ile Ile Asn Ile Ser Cys Val Lys Asn  
1 5 10 15

Asn Trp Ser Asn Asp Val Arg Ala Ser Leu Tyr Ser Leu Met Val Leu  
20 25 30

Ile Ile Leu Thr Thr Leu Val Gly Asn Leu Ile Val Ile Val Ser Ile  
35 40 45

Ser His Phe Lys Gln Leu His Thr Pro Thr Asn Trp Leu Ile His Ser  
50 55 60

Met Ala Thr Val Asp Phe Leu Leu Gly Cys Leu Val Met Pro Tyr Ser  
65 70 75 80

Met Val Arg Ser Ala Glu His Cys Trp Tyr Phe Gly Glu Val Phe Cys  
85 90 95

Lys Ile His Thr Ser Thr Asp Ile Met Leu Ser Ser Ala Ser Ile Phe  
100 105 110

His Leu Ser Phe Ile Ser Ile Asp Arg Tyr Tyr Ala Val Cys Asp Pro  
115 120 125

Leu Arg Tyr Lys Ala Lys Met Asn Ile Leu Val Ile Cys Val Met Ile  
130 135 140

Phe Ile Ser Trp Ser Val Pro Ala Val Phe Ala Phe Gly Met Ile Phe  
145 150 155 160

Leu Glu Leu Asn Phe Lys Gly Ala Glu Glu Ile Tyr Tyr Lys His Val  
165 170 175

His Cys Arg Gly Gly Cys Ser Val Phe Phe Ser Lys Ile Ser Gly Val  
180 185 190

Leu Thr Phe Met Thr Ser Phe Tyr Ile Pro Gly Ser Ile Met Leu Cys  
195 200 205

Val Tyr Tyr Arg Ile Tyr Leu Ile Ala Lys Glu Gln Ala Arg Leu Ile  
210 215 220

Ser Asp Ala Asn Gln Lys Leu Gln Ile Gly Leu Glu Met Lys Asn Gly  
225 230 235 240

Ile Ser Gln Ser Lys Glu Arg Lys Ala Val Lys Thr Leu Gly Ile Val  
245 250 255

Met Gly Val Phe Leu Ile Cys Trp Cys Pro Phe Phe Ile Cys Thr Val  
260 265 270

Met Asp Pro Phe Leu His Tyr Ile Ile Pro Pro Thr Leu Asn Asp Val  
 275 280 285

Leu Ile Trp Phe Gly Tyr Leu Asn Ser Thr Phe Asn Pro Met Val Tyr  
 290 295 300

Ala Phe Phe Tyr Pro Trp Phe Arg Lys Ala Leu Lys Met Met Leu Phe  
 305 310 315 320

Gly Lys Ile Phe Gln Lys Asp Ser Ser Arg Cys Lys Leu Phe Leu Glu  
 325 330 335

Leu Ser Ser

<210> 91  
 <211> 1696  
 <212> DNA  
 <213> H.Sapiens

<400> 91		
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ataattactc aaaaggtgat gacaatggcg cagggaggga tggtgacttg cctggagatg	120	
cacagcacccg tctctccat actcggtcat tcacaccatc attgattcac caggcaccac	180	
tccgtgtcca gcaggactct ggggacccca aatggacact accatggaag ctgacccggg	240	
tgccactggc cacaggcccc gcacagagct tggatgatgag gactcctacc cccaaagggtgg	300	
ctgggacacg gtcttcctgg tggccctgct gtccttggg ctgccagcca atgggtttagt	360	
ggcgtggctg gccggctccc aggccggca tggagctggc acgcgtctgg cgctgctcct	420	
gctcagcctg gccctctctg acttcttggt cctggcagca gccgccttcc agatcctaga	480	
gatccggcat gggggacact ggccgctggg gacagctgcc tgccgcttct actacttcct	540	
atggggcgtg tcctactcct ccggcctttt cctgctggcc gccctcagcc tcgaccgctg	600	
cctgctggcg ctgtgcccac actggtaccc tgggcaccgc ccagtccgccc tgccctctg	660	
ggtctgcgcc ggtgtctggg tgctggccac actcttcagc gtgccttggc tggcttccc	720	
cgaggctgcc gtctgggtt acgacctggt catctgcctg gacttctggg acagcgagga	780	
gctgtcgctg aggatgctgg aggtcctggg gggcttctgg cctttcttcc tgctgctcgt	840	
ctgccacgtg ctcacccagg ccacagcctg tcgcacactgc caccgccaac agcagccgc	900	
agcctgccgg ggcttcgccc gtgtggccag gaccattctg tcagcctatg tggcttgg	960	
gctgccctac cagctggccc agctgctcta cctggccttc ctgtgggacg tctactctgg	1020	
ctacactgctc tgggaggccc tggctactc cgactacctg atcctactca acagctgcct	1080	
cagcccccttc ctctgcctca tggccagtgc cgacccctccgg accctgctgc gctccgtgct	1140	

ctcgcccttc	gcggcagctc	tctgcgagga	gcggccgggc	agttcacgc	ccactgagcc	1200
acagacccag	ctagattctg	agggtccaac	tctgccagag	ccgatggcag	aggcccagtc	1260
acagatggat	cctgtggccc	agcctcaggt	gaaccccaca	ctccagccac	gatcgatcc	1320
cacagctcag	ccacagctga	accctacggc	ccagccacag	tccgatccca	cagcccagcc	1380
acagctgaac	ctcatggccc	agccacagtc	agattctgtg	gcccaagccac	aggcagacac	1440
taacgtccag	accctgcac	ctgctgccag	ttctgtgcc	agtccctgtg	atgaagcttc	1500
cccaacccca	tcctcgcatc	ctacccagg	ggccctttag	gacccagcca	cacccctgc	1560
ctctgaagga	gaaagccccca	gcagcaccccc	gccagaggcg	gccccggg	caggccccac	1620
gtgagggtcc	aggaacacgc	aggcccacca	gagcagtgaa	agagcccagg	gcagacagag	1680
gaaccagcca	gtcaga					1696

<210> 92  
 <211> 505  
 <212> PRT  
 <213> H.Sapiens

<400> 92

Leu	Ala	Trp	Arg	Cys	Thr	Ala	Pro	Ser	Leu	Pro	Tyr	Ser	Val	Ile	His
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Thr	Ile	Ile	Asp	Ser	Pro	Gly	Thr	Thr	Pro	Cys	Pro	Ala	Gly	Leu	Trp
							20		25					30	
Gly	Pro	Gln	Met	Asp	Thr	Thr	Met	Glu	Ala	Asp	Leu	Gly	Ala	Thr	Gly
							35		40				45		
His	Arg	Pro	Arg	Thr	Glu	Leu	Asp	Asp	Glu	Asp	Ser	Tyr	Pro	Gln	Gly
						50		55			60				
Gly	Trp	Asp	Thr	Val	Phe	Leu	Val	Ala	Leu	Leu	Leu	Gly	Leu	Pro	
					65		70		75					80	
Ala	Asn	Gly	Leu	Met	Ala	Trp	Leu	Ala	Gly	Ser	Gln	Ala	Arg	His	Gly
						85			90				95		
Ala	Gly	Thr	Arg	Leu	Ala	Leu	Leu	Leu	Ser	Leu	Ala	Leu	Ser	Asp	
					100		105						110		
Phe	Leu	Phe	Leu	Ala	Ala	Ala	Phe	Gln	Ile	Leu	Glu	Ile	Arg	His	
							115		120				125		
Gly	Gly	His	Trp	Pro	Leu	Gly	Thr	Ala	Ala	Cys	Arg	Phe	Tyr	Tyr	Phe
						130		135			140				
Leu	Trp	Gly	Val	Ser	Tyr	Ser	Ser	Gly	Leu	Phe	Leu	Leu	Ala	Ala	Leu
						145		150			155				160

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Ser Leu Asp Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly  
165 170 175

His Arg Pro Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val  
180 185 190

Leu Ala Thr Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala  
195 200 205

Val Trp Trp Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu  
210 215 220

Glu Leu Ser Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe  
225 230 235 240

Leu Leu Leu Val Cys His Val Leu Thr Gln Ala Thr Ala Cys Arg  
245 250 255

Thr Cys His Arg Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg  
260 265 270

Val Ala Arg Thr Ile Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr  
275 280 285

Gln Leu Ala Gln Leu Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser  
290 295 300

Gly Tyr Leu Leu Trp Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu  
305 310 315 320

Leu Asn Ser Cys Leu Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp  
325 330 335

Leu Arg Thr Leu Leu Arg Ser Val Leu Ser Ser Phe Ala Ala Leu  
340 345 350

Cys Glu Glu Arg Pro Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln  
355 360 365

Leu Asp Ser Glu Gly Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln  
370 375 380

Ser Gln Met Asp Pro Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln  
385 390 395 400

Pro Arg Ser Asp Pro Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln  
405 410 415

Pro Gln Ser Asp Pro Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln  
420 425 430

Pro Gln Ser Asp Ser Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln  
435 440 445

Thr Pro Ala Pro Ala Ala Ser Ser Val Pro Ser Pro Cys Asp Glu Ala  
450 455 460

Ser Pro Thr Pro Ser Ser His Pro Thr Pro Gly Ala Leu Glu Asp Pro  
465 470 475 480

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1413

<210> 94  
 <211> 419  
 <212> PRT  
 <213> H.Sapiens

&lt;400&gt; 94

Met Asp Thr Thr Met Glu Ala Asp Leu Gly Ala Thr Gly His Arg Pro  
 1 5 10 15

Arg Thr Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly Gly Trp Asp  
 20 25 30

Thr Val Phe Leu Val Ala Leu Leu Leu Gly Leu Pro Ala Asn Gly  
 35 40 45

Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly Ala Gly Thr  
 50 55 60

Arg Leu Ala Leu Leu Leu Ser Leu Ala Leu Ser Asp Phe Leu Phe  
 65 70 75 80

Leu Ala Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His Gly Gly His  
 85 90 95

Trp Pro Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe Leu Trp Gly  
 100 105 110

Val Ser Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu Ser Leu Asp  
 115 120 125

Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly His Arg Pro  
 130 135 140

Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val Leu Ala Thr  
 145 150 155 160

Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala Val Trp Trp  
 165 170 175

Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu Glu Leu Ser  
 180 185 190

Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe Leu Leu Leu  
 195 200 205

Leu Val Cys His Val Leu Thr Gln Ala Thr Ala Cys Arg Thr Cys His  
 210 215 220

Arg Gln Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg Val Ala Arg  
 225 230 235 240

Thr Ile Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr Gln Leu Ala  
 245 250 255

Gln Leu Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu

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260 265 270

Leu Trp Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser  
275 280 285

Cys Leu Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr  
290 295 300

Leu Leu Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu  
305 310 315 320

Arg Pro Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser  
325 330 335

Glu Gly Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met  
340 345 350

Asp Pro Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser  
355 360 365

Asp Pro Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser  
370 375 380

Asp Pro Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser  
385 390 395 400

Asp Ser Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln Thr Pro Ala  
405 410 415

Pro Ala Ala

<210> 95  
<211> 49  
<212> DNA  
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<220>  
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<400> 95  
ttcaaagctt atggaatcat ctttctcatt tggagtgatc cttgctgtc

49

<210> 96  
<211> 49  
<212> DNA  
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<400> 96  
ttcaactcgag ttagccatca aactctgagc tggagatagt gacgatgtg

49

<210> 97  
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 <212> DNA  
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 <223> Novel Sequence

<400> 97  
 gctcaaccca ctcatctatg cc

22

<210> 98  
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 <212> DNA  
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<220>  
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<400> 98  
 aaacttctct gcccttaccc tc

22

<210> 99  
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<400> 99  
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20

<210> 100  
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21

<210> 101  
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<212> DNA  
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<400> 101  
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28

<210> 102  
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<400> 102  
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30

<210> 103  
 <211> 30  
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<400> 103  
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30

<210> 104  
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<400> 104  
 cgtagagtgc acagatagcg gccaggatgc

30

<210> 105  
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<400> 105  
aaccggatca tctacacgc

19

<210> 106  
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<400> 106  
tgcctgtgga gccgctgg

18

<210> 107  
<211> 33  
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<400> 107  
gcataagctt ccatgtacaa cgggtcgtgc tgc

33

<210> 108  
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gcattctaga tcagtgccac tcaacaatgt ggg

33

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tgaaataacct gtccgcagcc	20
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<210> 112	
<211> 34	
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<221> misc_feature	
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<400> 113	

cagcccaaac atccaaagtc

19

<210> 114  
 <211> 19  
 <212> DNA  
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<220>  
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 <223> Novel Sequence

<400> 114  
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19

<210> 115  
 <211> 34  
 <212> DNA  
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<220>  
 <221> misc\_feature  
 <223> Novel Sequence

<400> 115  
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34

<210> 116  
 <211> 39  
 <212> DNA  
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<220>  
 <221> misc\_feature  
 <223> Novel Sequence

<400> 116  
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39

<210> 117  
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<400> 117  
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20

<210> 118  
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 <212> DNA  
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<400> 118  
ccgcaggagc aatgaaaatc ag

22

<210> 119  
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<400> 119  
ctgaaagttg tcgctgacc

19

<210> 120  
<211> 21  
<212> DNA  
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<400> 120  
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21

<210> 121  
<211> 25  
<212> DNA  
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<400> 121  
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25

<210> 122  
<211> 30  
<212> DNA  
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<220>  
<221> misc\_feature  
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<400> 122  
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30

<210> 123  
<211> 20  
<212> DNA  
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<220>  
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<223> Novel Sequence

<400> 123  
ctgtctctct gtcctttcc

20

<210> 124  
<211> 22  
<212> DNA  
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<220>  
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<400> 124  
gcaccgatct tcattgaatt tc

22

<210> 125  
<211> 22  
<212> DNA  
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<220>  
<221> misc\_feature  
<223> Novel Sequence

<400> 125  
acttcaaaca acttcataacc cc

22

<210> 126  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<223> Novel Sequence

<400> 126  
acacacagca tagtagcg

18

<210> 127  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<223> Novel Sequence

<400> 127  
cagagcttga tgatgaggac

20

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<210> 132		
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gcgttaatacg actcactata gggagacctg ccacactgat gcaactcc		48
<210> 133		
<211> 24		
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48

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&lt;400&gt; 162

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24

&lt;210&gt; 163

&lt;211&gt; 50

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

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&lt;223&gt; Novel Sequence

&lt;400&gt; 163

gcgttaatacg actcactata gggagaccgc acgccactct ttactatccc

50

&lt;210&gt; 164

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Novel Sequence

&lt;400&gt; 164

gcacaaaaca caattccata agcc

24

&lt;210&gt; 165

&lt;211&gt; 52

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Novel Sequence

&lt;400&gt; 165

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52

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&lt;211&gt; 23

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&lt;213&gt; Artificial Sequence

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22

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22

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ctatccaacg cactggtgct gctttgttgc gcctacagcg ctgagctccg cactcgagcc 180  
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ttccgccaag	tcctggccgg	catggtgcac	cggctgctga	agagaacccc	gcgcccagca	1020
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ccgcgcccag	cgtccaccca	caacggctct	gtggacacag	agaatgattc	ctgcctgcag	1140
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&lt;210&gt; 186

&lt;211&gt; 363

&lt;212&gt; PRT

&lt;213&gt; H.Sapiens

&lt;400&gt; 186

Met	Gly	Pro	Gly	Glu	Ala	Leu	Leu	Ala	Gly	Leu	Leu	Val	Met	Val	Leu
1					5				10				15		
Ala	Val	Ala	Leu	Leu	Ser	Asn	Ala	Leu	Val	Leu	Leu	Cys	Cys	Ala	Tyr
					20				25			30			
Ser	Ala	Glu	Leu	Arg	Thr	Arg	Ala	Ser	Gly	Val	Leu	Leu	Val	Asn	Leu
		35				40						45			
Ser	Leu	Gly	His	Leu	Leu	Leu	Ala	Ala	Leu	Asp	Met	Pro	Phe	Thr	Leu
		50				55					60				
Leu	Gly	Val	Met	Arg	Gly	Arg	Thr	Pro	Ser	Ala	Pro	Gly	Ala	Cys	Gln
		65			70				75			80			
Val	Ile	Gly	Phe	Leu	Asp	Thr	Phe	Leu	Ala	Ser	Asn	Ala	Ala	Leu	Ser
					85				90			95			
Val	Ala	Ala	Leu	Ser	Ala	Asp	Gln	Trp	Leu	Ala	Val	Gly	Phe	Pro	Leu
					100			105			110				
Arg	Tyr	Ala	Gly	Arg	Leu	Arg	Pro	Arg	Tyr	Ala	Gly	Leu	Leu	Gly	
					115			120			125				
Cys	Ala	Trp	Gly	Gln	Ser	Leu	Ala	Phe	Ser	Gly	Ala	Ala	Leu	Gly	Cys
					130			135			140				
Ser	Trp	Leu	Gly	Tyr	Ser	Ser	Ala	Phe	Ala	Ser	Cys	Ser	Leu	Arg	Leu
					145			150			155			160	
Pro	Pro	Glu	Pro	Glu	Arg	Pro	Arg	Phe	Ala	Ala	Phe	Thr	Ala	Thr	Leu
					165				170			175			
His	Ala	Val	Gly	Phe	Val	Leu	Pro	Leu	Ala	Val	Leu	Cys	Leu	Thr	Ser
					180			185			190				
Leu	Gln	Val	His	Arg	Val	Ala	Arg	Arg	His	Cys	Gln	Arg	Met	Asp	Thr
					195			200			205				
Val	Thr	Met	Lys	Ala	Leu	Ala	Leu	Ala	Asp	Leu	His	Pro	Ser	Val	

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210

215

220

Arg Gln Arg Cys Leu Ile Gln Gln Lys Arg Arg Arg His Arg Ala Thr  
225 230 235 240

Arg Lys Ile Gly Ile Ala Ile Ala Thr Phe Leu Ile Cys Phe Ala Pro  
245 250 255

Tyr Val Met Thr Arg Leu Ala Glu Leu Val Pro Phe Val Thr Val Asn  
260 265 270

Ala Gln Trp Gly Ile Leu Ser Lys Cys Leu Thr Tyr Ser Lys Ala Val  
275 280 285

Ala Asp Pro Phe Thr Tyr Ser Leu Leu Arg Arg Pro Phe Arg Gln Val  
290 295 300

Leu Ala Gly Met Val His Arg Leu Leu Lys Arg Thr Pro Arg Pro Ala  
305 310 315 320

Ser Thr His Asp Ser Ser Leu Asp Val Ala Gly Met Val His Gln Leu  
325 330 335

Leu Lys Arg Thr Pro Arg Pro Ala Ser Thr His Asn Gly Ser Val Asp  
340 345 350

Thr Glu Asn Asp Ser Cys Leu Gln Gln Thr His  
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29

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<400> 188

gcattctaga cctcagtggtg tctgctgc

28

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18